

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2004, 05:23:17 ; Search time 8805 Seconds

(without alignments)  
11214.184 Million cell updates/sec

Title: US-09-679-687B-1

Perfect score: 2088

Sequence: 1 gcacgagacactcctcacct.....aaaaaaaaaaaaaaaaaaaaa 2088

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_hcg.\*

3: gb\_in.\*

4: gb\_om.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_sts.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1320.6	63.2	1834	8	AB008464 Zea mays
2	1073.8	51.4	2021	8	AF408843 Triticum
3	1070.6	51.3	2134	8	AF408842 Triticum
4	1070.6	51.3	2160	8	BT009324 Triticum
5	1062.6	50.9	2044	8	HV0272309 Triticum
6	1058.8	50.7	2106	8	AF408844 Triticum
7	1053	50.4	2083	8	BT009233 Triticum
8	1021	48.9	2062	8	AK100027 Triticum
9	1016.8	48.7	2036	8	D87819 Oryza sativ
10	958.2	45.9	1580	6	AX653870 Sequence
11	812	38.9	1713	8	AB071809 Oryza sat
12	745.8	35.7	17340	2	AC149831 Zea mays
13	608.6	29.1	2036	8	AK073105 Oryza sat
14	603.8	28.9	1972	8	AB091674 Oryza sat
15	566	27.1	1222	8	AK109355 Oryza sat
16	474.6	22.7	1072	8	BT009200 Triticum
17	397	19.0	1830	8	AV137242 Oryza sat
18	395.4	18.9	2158	8	AB091673 Oryza sat
19	385.6	18.5	2166	8	AY581895 Zea mays

20	368.6	17.7	1800	8	PMA534442	Plantago
21	348.6	16.7	2386	8	AY098894	Citrus si
22	330.8	15.8	1638	6	AX654482	Sequence
23	327.2	15.7	1785	6	AX259876	Sequence
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25	327.2	15.7	1785	6	AX651257	Sequence
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27	323.6	15.5	2137	8	AF166498	Lyceopersi
28	316	15.1	2130	8	AF021809	Vitis vin
29	315	15.1	1818	6	AX259902	Sequence
30	315	15.1	1818	8	AY291289	Solanum t
31	300.2	14.4	2558	8	AK065430	Oryza sat
32	292.4	14.0	2018	8	HV0272308	Hordeum v
33	290.8	13.9	2135	6	AX306541	Sequence
34	284.2	13.6	1796	8	AB036758	Daucus ca
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36	276.2	13.2	173374	8	AC146340	Genomic s
37	276.2	13.2	305960	8	AE017092	Oryza sat
38	271.6	13.0	7518	8	AF419298	Oryza sat
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## ALIGNMENTS

RESULT 1  
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LOCUS AB008464 1834 bp mRNA linear PLN 23-MAY-2003  
DEFINITION Zea mays mRNA for Sucrose Transporter, complete cds.  
ACCESSION AB008464  
VERSION AB008464.1 GI:5771353  
KEYWORDS Sucrose Transporter.  
SOURCE Zea mays  
ORGANISM Zea mays

REFERENCE 1  
Aoki,N., Hirose,T., Takahashi,S., Ono,K., Ishimaru,K. and Ohsugi,R.  
Molecular cloning and expression analysis of a gene for a sucrose  
transporter in maize (Zea mays L.)  
Plant Cell Physiol. 40 (10), 1072-1078 (1999)

JOURNAL MEDLINE  
PUBMED 20058970  
REFERENCE 2 (bases 1 to 1834)

Aoki,N.  
Direct Submission  
Submitted (24-OCT-1997) Naohiro Aoki, Japan International Research  
Center for Agricultural Sciences, Biological Resources Division;  
1-2 Ohwashi, Tsukuba, Ibaraki 305, Japan  
(E-mail:naoki@res.jircas.affrc.go.jp, Tel:81-0298-38-6305,  
Fax:81-0298-38-6650)

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1600, Canberra, ACT 2601, Australia  
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ORIGIN

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Qy	247	GTCGCGCGCGCGCGCGGTGTGTGCACACAGTGGCCCCGATCAGCTCGCGGAGGCTCATC	306		
Db	181	GGCGCGCGCGCGCGGCGGACGCCGCCGCTGTGCACATCAGCTTCGGCAGGCTCATC	240		
Qy	307	CTCGCGCGCATGTCGCGCGCGGTGCAGTAGCGTGGCGCGGTGCAGTCTCCCTCCCTC	366		
Db	241	CTCGCGCGCATGTCGCGCGCGGTGCAGTAGCGTGGCGCGGTCCAGCTCTCCCTGCCTC	300		
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Qy	427	GGCCCTATTGCCCGCTTAGTGCTCCAAACCGCTGGTTGGCCTGTACAGCAGAGGTGACA	486		
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Qy	607	TGCAGCTCTACACAGGTCTCTGTTGGACAGCTGCGATCGTGACGTTCTGGGGTTTTGG	666		
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Db	601	CTCCTTGACTTCTCCAAACACACTGTGTSCAGGTCACAGCTCATATGATGGCTGATTTA	660		
Qy	727	TGTGACCATCATGGGCCAAGTGGCGGTAACTCCATCTTCTGTTCTTTGGATGGCGCTGGGA	786		
Db	661	TCAGCTCAACATGGAACCCAGTGCAGAAATTCATCTTCTGTCTTGGATGGCACTTAGGA	720		
Qy	787	AACATCTTAGCTACTCTCTGCTCCAGAACATTTGGCAACAATGGCAAGAAGTGTTCCCTTCCTT	846		
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Qy	847	AAACAGAGCCCTGCTGTGAGGCTGTGGCAACCTGAAAGGTGCAATTTCTGTGTGGCGCTG	906		

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Triticum.	1 (bases 1 to 2134)	Aoki, N., Whitfield, P.R., Hoeren, F., Scofield, G.N., Newell, K., Patrick, J., Offler, C., Clarke, B., Rahman, S. and Furbank, R.T.
Three sucrose transporter genes are expressed in the developing grain of wheat	2 (bases 1 to 2134)	Aoki, N., Whitfield, P.R., Hoeren, F., Scofield, G.N., Newell, K., Patrick, J., Offler, C., Clarke, B., Rahman, S. and Furbank, R.T.
Plant Mol. Biol. (2002) In press	2 (bases 1 to 2134)	Direct Submission
Division of Plant Industry, CSIRO, GPO BOX 1600, Canberra, ACT 2601, Australia	Location/Qualifiers	
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DB	279	GCGCGCGCGCGCGCGGCGGAGCGCCCGCGGTGAGACATCAGCTCGGAGGCTCATC 338
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DB	459	GSCCCTATTGCGGCTTAGTGTGCTCAACCGCTGTGGCTGTGACGACGAGGTGATCA 518
QY	487	TCGAGATGGGAGAGCGAGGCGGCTTATCTGACAGGCTGCATGCTCATCTGCGTTGCC 546
DB	519	TCAAGATGGGAGAGCGAGGCGGCTTATCTGACAGGCTGCATGCTCATCTGCGTTGCC 578
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ORIGIN

QY	667	CTCCTTGACTTCTCCAAACAACACTGTGAGGGTCCAGCAGTGTATGATGGCTGATCTA 726
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QY	727	TGTGACCATCATGGCCAAAGTGGCTAACTCCATCTTCTGTTCTTGTGATGGCTGGGA 786
DB	759	TAGCCCCAGCATGAGCCAGTGCAGCAATTAATCTTCTGTTCTTGTGATGGCTGGGA 818
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LOCUS Triticum aestivum clone wlm24.pk0015.gll.fis, full insert mRNA
DEFINITION
sequence.
ACCESSION
BT009324
VERSION G1:32128875
KEYWORDS
SOURCE
ORGANISM
Triticum aestivum (bread wheat)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
REFERENCE
1 (bases 1 to 2160)
Tingey,S.V., Wolters,P., Powell,W., Dolan,M., Miao,G.-H.,
Caraher,N.R., Hanafey,M.K. and Hainey,C.F.
Direct Submission
Submitted (20-JUN-2003) Crop Genetics, E. I. DuPont de Nemours and
Company, 1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104,
USA
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Best Local Similarity 79.8%; Pred. No. 11e-140;
Matches 1275; Conservative 0; Mismatches 319; Indels 3; Gaps 1;
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QY 367 ACGCCCTAGTCAGACTCTGGGGCTTTCAATGCGCTCACTTCAATGAGCTCTGC 426
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377 ACCCCCTAGTCCAGACTGGGACTTTTCGATGCTCTGACTTCAATTCATGAGCTCTGC 436
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677 CTCCTTGACTTCTCAACAACTGTGAGGCTCAGCACTGCTATGATGGCTGATTTA 736
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RESULT 5  
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LOCUS  
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ACCESSION                  AJ272309  
VERSION                     AJ272309.1    GI:7024414  
KEYWORDS                    sucrose transporter; suc1 gene.  
SOURCE                      Hordeum vulgare subsp. vulgare  
ORGANISM                    Hordeum vulgare subsp. vulgare  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poideae; Triticeae; Hordeum.

1  
Weschke,W., Panitz,R., Sauer,N., Wang,Q., Neubohn,B., Weber,H. and  
Wobus,U.  
TITLE  
Sucrose transport into Barley Seeds: Molecular Characterisation of  
two Transporters and Implications for Seed Development and Starch  
Accumulation  
Unpublished  
2 (bases 1 to 2044)  
Weschke,W.  
DIRECT SUBMISSION  
Submitted (21-FEB-2000) Weschke W., Molecular Genetics, Institut  
fuer Pflanzengenetik und Kulturpflanzenforschung, Corrensstr.3,  
Gatersleben 06466, GERMANY

FEATURES  
source  
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ORIGIN  
Query Match                      50.9%;    Score 1062.6;    DB 8;    Length 2044;  
Best Local Similarity            80.0%;    Pred. No. 1.4e-139;  
Matches 1277; Conservative      0; Mismatches 314; Indels    6; Gaps    2;

Qy	183	CCGTACGTTGTGTCGTCGCATGGCTCGTGCGCACGGCGGCGAGCTGGCGGAGCTGTGCGG	242
Dd	124	CCCTCCGATGCGCGGGCGCGCGCAACCGCGAGTGGAGCTCTCGTGGGGGTTCGGCGG	183
Qy	243	GGGGGTCCGCGCGGGCGCGCG---GTGGTAGCACGTGCCGCCCATCAGCCTCGGGAG	299
Dd	184	CAGAGCGGGCGCGCGAGCGCGCGAGAGCGCGCGAACCCCGCTGTGAGATCAGCCTCGGAG	243
Qy	300	GCTCATCTCCCGGCATGTCGCGCGGGCGGTGCAGTACCGETGGGCGCTGCAGCTCTC	359
bh	244	GCTCATCTCCCGGCATGTCGCGCGGGCGGTGCAGTACGATGGGCGCTCCAGCTCTC	303





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Db      1300 GTTCAGCTCGTTCTGATCGAGCGCTGTGCAAGAGGCTAGCGCCGCGGTGTGGT 1359
Qy      1320 GACGAGCAACTTATGTCTGCTGCGTCAGTGGCGGCCACCGCGTGTATGCTTCTGGTC 1379
Db      1360 GTGAGCAACTTCTCTGCTGCTCTCTCATGGCGCGATTGGAATATAAGCTTGTGGGC 1419
Qy      1380 GCTCAGGCACTACCAAGGCTAGTGCAGAGCGCCATCACCGGAAACCCAGCATCAAGGC 1439
Db      1420 TACTCAGGCACTTCATGGGTATATCCAGCACGCCATCACCGCCAGCAAGAGATCAAGAT 1479
Qy      1440 GGTGCGCTGCTCTCTCTGCTGCTGCTGCGGCGTCCCTCTGCGCATCTGTACAGCGTCCC 1499
Db      1480 GGTCTCCCTCGCTCTCTCTGCTGCTGCTGCGGAAATCCCTCTGCGCATCTGTACAGTGTCCC 1539
Qy      1500 GTTTCGCGTGTACGCGGCTAGTGGCGGCGCACCGCGGCGGCGGAGGCGGTGTGCACCGG 1559
Db      1540 TTTTCGCGTGTACGCGGCTAGTGGCGGCGAGAGAGCGGTGGCCAGGCTGTGCACGGG 1599
Qy      1560 GGTCTCTCAACTCTCATCTGCTATCCCTCAGGTGATCATCGCGTGTGGCGCGCGCGCGTG 1619
Db      1600 GGTCTCAACTCAGCTGCTGCTATCCCAAGGCTGATCATCGCGTGTGGCGCGCGCGCGTG 1659
Qy      1620 GGACGCGTGTTCGCGAAGGCGCAATCCCGCGTGTGGCGTGTGGCGCTTCGCGCT 1679
Db      1660 GGACGCGTGTTCGCGAAGGCGCAATCCCGCGTGTGGCGTGTGGCGCTTCGCGCT 1719
Qy      1680 GGTTCGCGGCGGTGTGGCGGCTGTTCCTGCTGCCAAGATCTCCAAAGCGCGATTCGCGGC 1739
Db      1720 CATCGCGGCGCTGTGGCGGCTATCTCTGCTGCCAAGATCTCCAGGCGCGATTCGCGGC 1779
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RESULT 7
LOCUS   BT009233
DEFINITION   2083 bp mRNA linear PLN 20-JUN-2003
            Triticum aestivum clone wleln.pk0103.c11:fls, full insert mRNA
            sequence.
ACCESSION   BT009233
VERSION     BT009233.1 GI:32128784
KEYWORDS    FLI CDNA.
SOURCE      Triticum aestivum (bread wheat)
ORGANISM    Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Pooideae; Triticeae; Triticum.
REFERENCE   1 (bases 1 to 2083)
AUTHORS     Tingey,S.V., Wolters,P., Powell,W., Dolan,M., Miao,G.-H.,
            Caraher,N.R., Hanafey,M.K. and Hainey,C.F.
TITLE       Direct Submission
JOURNAL     Submitted (20-JUN-2003) Crop Genetics, E. I. DuPont de Nemours and
            Company, 1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104,
            USA
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ORIGIN
Query Match      50.4%; Score 1053; DB 8; Length 2083;
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Matches 1249; Conservative 0; Mismatches 306; Indels 3; Gaps 1;

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Db      329 ACTCATCTCCGCGGCAATGTCGCGCGCGCGGTGCAAGTACGATGGCGGCTCCAGCTCTC 388
Qy      360 CCTCTCAGCGCCCTACGTGCGAGCTCTGGGCTTTTCAATCGCTCACTTCAATCAATGTG 419
Db      389 CCTGCTCACCCCTACGTGCGAGCTCTGGACTTTCGATGCTCTGACTTCAATCAATGTG 448
Qy      420 GCTTCGCGCCCTATGTCGCGCTTAGTGTCAACCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 479
Db      449 GCTCTGCGCGCCCTATGTCGATTTAGTGTTCACCATGCGTGTGGCTCTACAGTGACAA 508
Qy      480 GTGTACATCGAGATGGGAGACGAGGCGCTTTATCTCTGACAGGCTGCTCTAGGGACACGAA 539
Db      509 GTGCACATCTAGATGGGAGACGACGACCGTTCATCTGACAGGATCACTCTCATCTG 568
Qy      540 CTTTCGCGCTCATGTTGTGCGATTTCTGTCAGACATCGAGCTGCTTAGGGACACGAA 599
Db      569 CATTCGCTGTGTGCTGCTGCGCTTCTCGCTGACATTCGAGCTGCTTGGGTGACAGAA 628
Qy      600 GGAACATGCGAGCTCTACCGGCTCTCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 659
Db      629 GGAAGAGTGCAGTCTCTATCATGCGCTCTGTCGACCGCTGCAATTTGATGATGCTTGG 688
Qy      660 GTTTGGCTCTTGTGATCTTCTCAACAACTGTGCGGCTGCGACAGCTGCTATGATGCG 719
Db      689 ATTCTGGCTCTTGTGATCTTCTCAACAACTGTGCAAGTCCAGCGCTGCTCTGATGCG 748
Qy      720 TGATCTATGTGACCATCATGCGGCTGCGCTAACTCCATCTTCTCTCTTCTTCTGATGCG 779
Db      749 TGATTTATCAGCTGAGCTGAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAG 808
Qy      780 GTTGGGAAACATCTAGGCTACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 839
Db      809 GCTAGGAAATATCTTGGATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 868
Qy      840 CTTCTCTTAAACAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 899
Db      869 GTTCTCTCCGACAAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 928
Qy      900 GCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 959
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Qy      960 GTACAGAGCAAGAGAACTCTCCGACGACGAGGCGCGCGCGGAGTCTGAGACTGAGCG 1019
Db      989 GTACAAAGGCGATTGCGCGCTCC---CAACAAAGGCGCAATGCGCGAGTGAAGTCGAGCG 1045
Qy      1020 TACCGGCGCACTTTCGCTGCTCAAGGCTTCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1079
Db      1046 CACCGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1105
Qy      1080 GCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1139
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Qy      1140 CTGGATGGCGCGGAGATCTACCGGCGACCCCAAGGCGAGCAACCGCGAGATCTCGCG 1199
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 1804 GCGGC 1808

RESULT 9  
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 LOCUS  
 DEFINITION  
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 ACCESSION  
 D87819  
 VERSION  
 D87819.1  
 KEYWORDS  
 GI:2723470  
 sucrose transporter.  
 SOURCE  
 Oriza sativa (japonica cultivar-group)  
 ORGANISM  
 Oriza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzoideae; Oryza.  
 REFERENCE  
 1  
 HIROSE,T., IMAIZUMI,N., SCOFIELD,G.N., FURBANK,R.T. and OHSUGI,R.  
 cDNA cloning and tissue specific expression of a gene for sucrose transporter from rice (Oriza sativa L.)  
 Plant Cell Physiol. 38 (12), 1389-1396 (1997)  
 JOURNAL  
 MEDLINE  
 98182940  
 PUBMED  
 9522469  
 REFERENCE  
 2 (bases 1 to 2036)  
 HIROSE,T.  
 Direct Submission  
 Submitted (09-SEP-1996) Tatsuhiro Hirose, Hokuriku National Agricultural Experiment Station, Lab. of Rice Metabolism; 1-2-Iinada, Joetsu, Niigata 943-01, Japan  
 (E-mail:dragon@affrc.go.jp, Tel:0255-26-8300, Fax:0255-24-8578)  
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gene  
 CDS

Query Match 45.9%; Score 958.2; DB 6; Length 1580;  
Best Local Similarity 77.4%; Pred. No. 6.4e-125;



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Query Match 38.9%; Score 812; DB 8; Length 1713;  
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QY 427 GGCCTATTGCGGCTTAGTGTCCAAAGCGTGGTGGCTGTACAGGACAGGTTGACA 486  
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QY 1738 GCGTCAAGC 1747  
 DB 1588 ATGCGCGCGC 1597

## RESULT 12

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 DEFINITION AC149831 173340 bp DNA linear HTG 22-JUN-2004  
 AC149831  
 VERSION AC149831.1 GI:49035059  
 KEYWORDS HTG; HTGS\_PHASE1; HTGS\_FULLTOP; HTGS\_ACTIVEFIN.  
 SOURCE Zea mays  
 ORGANISM Zea mays

REFERENCE 1 (bases 1 to 173340)  
 AUTHORS Birren, B., Nusbaum, C., Lander, E., Butler, E., Wing, R., Bhatti, A.K., Messing, J., Abouelleil, A., Allen, N., Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhalter, S., Camarata, J., Chang, J., Choepel, Y., Collymore, A.,

REFERENCE 2 (bases 1 to 173340)  
 AUTHORS Birren, B., Nusbaum, C., Lander, E., Butler, E., Wing, R., Bhatti, A.K., Messing, J., Abouelleil, A., Allen, N., Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhalter, S., Camarata, J., Chang, J., Choepel, Y., Collymore, A.,

REFERENCE 3 (bases 1 to 173340)  
 AUTHORS Birren, B., Nusbaum, C., Lander, E., Butler, E., Wing, R., Bhatti, A.K., Messing, J., Abouelleil, A., Allen, N., Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhalter, S., Camarata, J., Chang, J., Choepel, Y., Collymore, A.,

REFERENCE 4 (bases 1 to 173340)  
 AUTHORS Birren, B., Nusbaum, C., Lander, E., Butler, E., Wing, R., Bhatti, A.K., Messing, J., Abouelleil, A., Allen, N., Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhalter, S., Camarata, J., Chang, J., Choepel, Y., Collymore, A.,

REFERENCE 5 (bases 1 to 173340)  
 AUTHORS Birren, B., Nusbaum, C., Lander, E., Butler, E., Wing, R., Bhatti, A.K., Messing, J., Abouelleil, A., Allen, N., Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhalter, S., Camarata, J., Chang, J., Choepel, Y., Collymore, A.,







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source

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AB091674  
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Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)  
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Aoki,N., Hirose,T., Scofield,G.N., Whitfield,P.R. and Furbank,R.T.  
The sucrose transporter gene family in rice  
Plant Cell Physiol. 44 (3), 223-232 (2003)  
2255500  
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2 (bases 1 to 1972)  
Hirose,T., Aoki,N., Scofield,G.N., Whitfield,P., Furbank,R.T. and  
Terao,T.  
Direct Submission  
Submitted (13-SEP-2002) Tatsuro Hirose, National Agricultural  
Research Center, Department of Rice Research; 1-2-1 Inada, Joetsu,  
Niigata 943-0193, Japan (E-mail:dragon@affrc.go.jp,  
Tel:81-25-526-8300, Fax:81-25-524-8578)  
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Query Match 28.9%; Score 603.8; DB 8; Length 1972;  
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Matches 956; Conservative 0; Mismatches 497; Indels 24; Gaps 3;

QY 289 AGCTCGGGAGGCTCATCTCGCGCATGCTGCTCGCGCGCGCTGCTGCTGCTGCTGCTGCTG 348  
Db 159 AGGATCGTGGCTGTTCTTCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 218





GenCore version 5.1.6  
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(without alignments)  
8022.309 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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3	187.8	9.0	1773	1 US-08-356-340-3	Sequence 3, Appli
4	187.8	9.0	1773	2 US-08-786-585-3	Sequence 3, Appli
5	72.2	3.5	7724	4 US-08-486-049-1	Sequence 1, Appli
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7	71.4	3.4	4456	3 US-09-095-443-1	Sequence 1, Appli
8	71.4	3.4	10288	4 US-09-845-917A-28	Sequence 28, Appl
9	71.4	3.4	13414	4 US-09-845-917A-27	Sequence 27, Appl
10	71.2	3.4	2845	4 US-10-140-002-207	Sequence 207, App
11	70.8	3.4	1069	3 US-09-372-422A-7	Sequence 7, Appli
12	70.8	3.4	2806	4 US-09-653-839-9	Sequence 9, Appli
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23	69.8	3.3	1725	4 US-09-668-097A-21	Sequence 21, Appl
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C 30	69.2	3.3	396	4 US-09-970-966-10	Sequence 10, Appl
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C 34	69	3.3	2730	4 US-09-252-991A-13932	Sequence 13932, A
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C 45	69	3.3	3410	4 US-09-688-489-110	Sequence 110, App

# ALIGNMENTS

RESULT 1  
US-08-356-340-1  
; Sequence 1, Application US/08356340  
; Patent No. 5608146  
; GENERAL INFORMATION:  
; APPLICANT: FROMMER, Wolf-Bernd  
; APPLICANT: RIESMEIER, Jorg  
; TITLE OF INVENTION: DNA SEQUENCES WITH OLIGOSACCHARIDE  
; TITLE OF INVENTION: TRANSPORTER, PLASMIDS, BACTERIA AND PLANTS CONTAINING A  
; TITLE OF INVENTION: TRANSPORTER AS WELL AS A PROCESS FOR THE PREPARATION AND  
; TITLE OF INVENTION: TRANSFORMATION OF YEAST STRAINS FOR THE IDENTIFI...  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Ostrolenk, Faber, Gerb & Soffen  
; STREET: 1180 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: US  
; ZIP: 10036-8403  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION NUMBER: US/08/356,340  
; APPLICATION NUMBER: US/08/356,340  
; FILING DATE: 21-DEC-1994  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US PCT/EP93/01604  
; FILING DATE: 22-JUN-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DE P42 20 759.2  
; FILING DATE: 24-JUN-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meilman, Edward A.  
; REGISTRATION NUMBER: 24,735  
; REFERENCE/DOCKET NUMBER: P/951-106  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 382-0700  
; TELEFAX: (212) 382-0888  
; TELEX: 236925  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1969 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; ORIGINAL SOURCE:





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## RESULT 3

US-08-356-340-3

; Sequence 3, Application US/08356340

; Patent No. 5608146

; GENERAL INFORMATION:

; APPLICANT: FROMMER, Wolf-Bernd

; APPLICANT: RIESMEIER, Joerg

; TITLE OF INVENTION: DNA SEQUENCES WITH OLIGOSACCHARIDE

; TITLE OF INVENTION: TRANSPORTER, PLASMIDS, BACTERIA AND PLANTS CONTAINING A

; TITLE OF INVENTION: TRANSPORTER AS WELL AS A PROCESS FOR THE PREPARATION AND

; TITLE OF INVENTION: TRANSFORMATION OF YEAST STRAINS FOR THE IDENTIFI...

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Ostrolenk, Faber, Gerb &amp; Soffen

; STREET: 1180 Avenue of the Americas

; CITY: New York

; STATE: NY

; COUNTRY: US

; ZIP: 10036-8403

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/356,340

; FILING DATE: 21-DEC-1994

; CLASSIFICATION: 800

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: US PCT/EP93/01604

; FILING DATE: 22-JUN-1993

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: DE P42 20 759.2

; FILING DATE: 24-JUN-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Meilman, Edward A.

; REGISTRATION NUMBER: 24,735

; REFERENCE/DOCKET NUMBER: P/951-106

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 382-0700

; TELEFAX: (212) 382-0888

; TELEX: 236925

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1773 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; ORIGINAL SOURCE:

; ORGANISM: Solanum tuberosum

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 5..1552

; OTHER INFORMATION: /note= "Sucrose-Transporter"

US-08-356-340-3

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Best Local Similarity 48.8%; Pred. No. 9.5e-27;  
Matches 714; Conservative 0; Mismatches 707; Indels 42; Gaps 6;

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DB 710 AGCTTAAACAACATAGCTTAACCTTAGTCCGGGAAACAGAGCTCCCGGAGAAAGACGAG 769  
QY 976 AACCTCCGACACAGAGCGCGCGAGTCCGAGCTGAGCTACGCGCCACTGCGGCCACTTGC 1035  
DB 770 CAAGAAATCGACGAGAAATAGCCGGCGCGGAAATCATGAAGTACCGTTTTTCGGTAA 829  
QY 1036 GTGCTCAAGGGCTTCAAGGACCTGCTCCCGGGATGCGCTCGCTCTCTCGTACTGCC 1095  
DB 830 ATTTTGGGGCTTTGAAAGATTTACCTCGACCGATGTGGAATCTTATTAGTAACCTGT 889  
QY 1096 ATCAGCTGCTTCTGCTGCTCCGTTTCCGTTTCACTCTACGACAGCTGATGGCGCGGAG 1155  
DB 890 TTGAATCGATCGCTGCTTCCCTTTTCTTATACGATACAGATGTGATGCTTAAGAG 949  
QY 1156 ATCTACACCGGCAACCCAAAGGGAGCAACGCCAGATCTCGGGTTTCAAGAGAGTGT 1215  
DB 950 GTTTTCGGTGACAGTGGTATCGGATCGGAG-----GTGTACGATTTGGGTGA 997  
QY 1216 CGAGTCGGCGCTTGGGCTGCTACTCACTCGGTTATTTAGGGTTGAGCTCTGTTCTGT 1275  
DB 998 CGCGTGTGCAATGGGATTTACTGTGCAATCTGTGCTTGTAGGGTTTATGCTCACTTGG 1057

RESULT 4

US-08-786-555-3  
Sequence 3, Application US/08786555B  
Patent No. 5981181

GENERAL INFORMATION:  
APPLICANT: FROMMER, Wolf-Bernd

APPLICANT: RIESMEIER, Jorg  
TITLE OF INVENTION: DNA SEQUENCES WITH OLIGOSACCHARIDE TRANSPORTER,

TITLE OF INVENTION: PLASMIDS, BACTERIA AND PLANTS CONTAINING A TRANSPORTER  
TITLE OF INVENTION: AS WELL AS A PROCESS FOR PREPARATION AND TRANSFORMATION

TITLE OF INVENTION: OF YEAST STRAINS FOR THE IDENTIFICATION  
FILE REFERENCE: Frommer

CURRENT APPLICATION NUMBER: US/08/786,555B  
CURRENT FILING DATE: 1997-01-21

EARLIER APPLICATION NUMBER: 08/356,340  
EARLIER FILING DATE: 1994-12-21

EARLIER APPLICATION NUMBER: PCT/EP93/01604  
EARLIER FILING DATE: 1993-06-22

EARLIER APPLICATION NUMBER: DE P4220759.2  
EARLIER FILING DATE: 1992-06-24

NUMBER OF SEQ ID NOS: 11  
SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 3  
LENGTH: 1773

TYPE: DNA  
ORGANISM: Spinacia oleracea

US-08-786-555-3

Query Match 9.0%; Score 187.8; DB 2; Length 1773;  
Best Local Similarity 48.8%; Pred. No. 9.5e-27;  
Matches 714; Conservative 0; Mismatches 707; Indels 42; Gaps 6;

QY 265 GTGGTGACACGCTGGCCCGCATCAGCTCGGAGGCTCATTCTCGCGGATGTGCC 324  
DB 65 GTGAACAGCCTTTAGCACCACCAAGCTATGGAATAATTAGTTGAGCTTCCATAGCT 124  
QY 325 GCGCGCTGTCAGTACGGCTGGCGCTGCGAGCTCTCCCTCTCAGCCCTCAGTGCAGACT 384  
DB 125 GCTGGTGTCAATTTGGTGGGCTCTTCACTCTCTTGTCTTACACCTTATGTTCAATTG 184

QY 385 CTGGGCTTTTCATCGCGCTCACTTCATTCATGCTGCTCGGCGCCCTATTCCCGCTTA 444  
Db 185 CTCGGAATTCCTCATAAATTTGCTCTTTTATTTGGCTTTTGGACCGATTTCTGGTATG 244  
QY 445 GTGGTCAAACCGCTGGTGGCTGTACAGCAGAGGTGTACATCGAGATGGGGAGAGCG 504  
Db 245 ATTGTTACGCCAGTTGTGCGGTACTACAGTGATAATTTGCTCTCCGTTTGGTCCGCCG 304  
QY 505 AGCGCGTTTATCTGACAGGGTGCATGCTCACTCGGTTGCGGTCAATGTTGTTCGATTTC 564  
Db 305 CGGCCAATTCATTGCCCGCGAGTGCACCTTGTTATGATTGGGTTTTCTCATCGGATTC 364  
QY 565 TCGTCAGACATCGAGCTCTCTAGGGGACAGAAAGAACACTGCAGCGCTTACACAGGT 624  
Db 365 GCGCGCAGCTTGGTCAAGCCCTCCGTTGACAC-----TCTCGAAAGGA 409  
QY 625 CCGTGTGGCAGCTGCGATCTGTGTACGTTCTGGGGTTTTGGCTCTCTGACTTCTCCAAC 684  
Db 410 TTTAAGCCACGTGCCATTGCCCGTTTTTGTGCTCGGTTTTTGGATCTCTGATGTTGCTAAC 469  
QY 685 AACACTGTCCAGGTCACAGCGTGTATGATGGTGTATGATGACCATCATG----- 739  
Db 470 AACATGTTACAGGCCCATCGAGAGCACTACTGGTGTATCTCTCGGCGGAAATCCGCG 529  
QY 740 -GGCAAAGTGGCGTAACCTCACTCTGTTCTTGGATGGCGCTGGGAAACATCTAGGC 798  
Db 530 AGGATGAGAACAGCAAAATGCTTTTTCTCATCTTCATGGCGTCCGAAACATTTCTGGG 589  
QY 799 TACTCTCTGGCTCCAGCAAAATTTGGCAAGTGGTTCTCTTCTTAAACAGCGCC 858  
Db 590 TACGGCGCGGTTTATTTCTCACTCTTTAAAGTATTCCCTTTCTCAAAACCAAGCC 649  
QY 859 TCGTGTAGCGCTGTGCGAACCTGAAAGTGCATTTCTGGTGGCGGTGTCTCTAGTC 918  
Db 650 TCGCACATGTACTGCGCAATCTGAAGAGTTGTTCTTCACTGCTATTTCTCTTTACTC 709  
QY 919 CTGTGCTGACGGTAACCTGATCTTTCGCAAGAGGTGCGGTACAGAGCA---ACGAG 975  
Db 710 AGCTTAAACACCATAGCTTAACTTACTTCGCGGAAACAGAGCTCCCGAGAAAGACGAG 769  
QY 976 AACCTCCGACGACGAAGCGCGCGGAGGTGAGAGCTGAGCTTACCGGCCACTTGCC 1035  
Db 770 CAAGAAATCGACGAGAAATTAGCGCGCGCGGAAATCGAAAGTACCGTTTTTCGGTGA 829  
QY 1036 GTGCTCAAGGGTTCAAGACCTGCTCCGCGGATGCGGTCCGTCTCTCTGTAAGTCC 1095  
Db 830 ATTTTGGGGCTTTGAAAGAAATTAACCTCGACCGATGTGGATTCTTCTATTAGTAACCTGT 889  
QY 1096 ATCACTGCTTTCTGTGTTCCGTTTCATCTCTACGACCGAGCTGATGGATGGCGCGGAG 1155  
Db 890 TTGAATGATCGCGTGGTTCCCTTTTCTTATACGATACAGATTGGATGGCTAAGAG 949  
QY 1156 ATCTACACGGCGACCCCAAGGGAGAACGCCAGATCTCGGGTTTCAACGAAGGTGTC 1215  
Db 950 GTTTTCGGTGAACAAGTCGGTGATCGAG-----GTTGTACGATTTGGGTGA 997  
QY 1216 CGAGTGGCGCTTCGGGCTGTACTCACTCGGTTATTCTAGGTTTACGCTCTTCTG 1275  
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QY 1276 ATCGAGCCCATGTGCGGAAGTCCGGC---CGAGGGTGGTGTGGGTGACGAGCACTTC 1332  
Db 1058 GTTGAATTTTAGGGAAGAGATTTGGTGTGCTAAGAGTTATGGGNAATTTTGAATTT 1117  
QY 1333 ATGTCGTGGTGGCATCGGCGCACCGCGGTGATCAGCTTCTGTGCTCAGGAGTAC 1392  
Db 1118 GTTTGGCTATTGCTGCTATGACCAATTTTGGTCAACAAATCGCCGAGAAATCTCG 1177  
QY 1393 CACGGGTACGTGACGAGCGCATACCG---CGAACGCCAGCATCAAGCGCGTCTGCTC 1449  
Db 1178 CAGCAGACCCCGCGGACACTATGCGGCGGACCGCTGTGTTAAATCGTGCCTTG 1237

QY 1450 GTCTCTTCGCTTCCTGGGGTCCCTCTCTCGCATCTCTGTACAGCGTCCGCTTCGCGGTG 1509  
Db 1238 CTTCTCTTTGCCCGCTTGGTATTCCTCTTTGCGGCAACTTTTAGTATTCATTTGCTTTG 1297  
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Db 1298 GCATCTATATTTCTAGTAATCGTGGTTTACAGGACAAGTTTGTACCTAGAGTCTCAAT 1357  
QY 1570 ATCTCATGTCATCCCTCAGGTGATCATCGCGTGGCGCGCGCGCTGGAGCGCGCTG 1629  
Db 1358 CTTGCAATTTGTACACAGATGTTGGTGTCTACTAGTAGAGGGCCATGGGATGTTG 1417  
QY 1630 TTCGGAAGGCGCAACATCCCGGCTTTCGGGTGCGGTGCGCTTCGCGCTCTGTCGGCGC 1689  
Db 1418 TTTGAGAGAGAACTTGCCTGGATTTGTAGTTGGAGCAGTTGCGAGCTGCGCGCGCT 1477  
QY 1690 GTCGTGGCGGTTCCTGCTGCC 1712  
Db 1478 GTTTAGCACTCAATGTTGCC 1500

RESULT 5  
US-08-486-049-1  
; Sequence 1, Application US/08486049  
; Patent No. 6572862  
; GENERAL INFORMATION:  
; APPLICANT: Estes, Mary K  
; APPLICANT: Jiang, Xi  
; APPLICANT: Graham, David Y  
; TITLE OF INVENTION: Methods and Reagents to Detect and  
; TITLE OF INVENTION: Characterize No. 6572862walk and Related Viruses  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fulbright & Jaworski L.L.P.  
; STREET: 901 Pennsylvania Ave., N.W.  
; CITY: Washington, D.C.  
; STATE:  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/486,049  
; FILING DATE: June 7, 1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Davis, Peter  
; REGISTRATION NUMBER: 36,119  
; REFERENCE/DOCKET NUMBER: 311.023  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-662-0200  
; TELEFAX: 202-662-4643  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7724 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: unknown  
; MOLECULE TYPE: cDNA  
; ORIGINAL SOURCE:  
; ORGANISM: No. 6572862walk virus  
; STRAIN: 8FIIa  
; INDIVIDUAL ISOLATE: 8FIIa  
; IMMEDIATE SOURCE:  
; CLONE: pUCNV-953 and its derivatives  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 146..539  
; OTHER INFORMATION: /note= "The protein encoded by

OTHER INFORMATION: nucleotides 146 through 5359 is eventually cleaved  
OTHER INFORMATION: to make at least a picornavirus 2c-like protein, a  
OTHER INFORMATION: 3C-like protease and an RNA-dependent RNA polymerase.

FEATURE:  
NAME/KEY: CDS  
LOCATION: 5346..6935  
OTHER INFORMATION: /note= "Nucleotides 5346 through  
OTHER INFORMATION: 5359 are used for coding two different amino acid  
OTHER INFORMATION: sequences: the first is the sequence coded by  
OTHER INFORMATION: nucleotides 146 through 5359, the second by nucleotides  
OTHER INFORMATION: 5346 through 6935.

FEATURE:  
NAME/KEY: CDS  
LOCATION: 6938..7573  
US-08-486-049-1

Query Match      3.5%; Score 72.2; DB 4; Length 7724;  
Best Local Similarity      71.4%; Pred. No. 0.00012;  
Matches      95; Conservative      0; Mismatches      38; Indels      0; Gaps      0;  
QY      1956 TGTAGTAGTACAACTAGACGATGATGTTCCATCATCTTTGCTTTTATACATACCGTTT 2015  
Db      7577 TGTGTATATCAATGTCGGCATCATATTCATTTAATTAAGTTTAAATTT 7636  
QY      2016 TCTATTGCTTTAAAAA 2088  
Db      7637 GATGTTAAAAA 7709  
QY      2076 AAAAAA 2088  
Db      7697 AAAAAA 7709

RESULT 6  
5168051-9  
Patent No. 5168051  
APPLICANT: DERYNCK, RIK M.A.; GOEDEL, DAVID V.  
TITLE OF INVENTION: NUCLEIC ACID ENCODING TGF-B ITS USES  
NUMBER OF SEQUENCES: 21  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/389,929  
FILING DATE: 04-AUG-1989  
SEQ ID NO: 9:  
LENGTH: 2671  
5168051-9

Query Match      3.4%; Score 71.6; DB 6; Length 2671;  
Best Local Similarity      81.4%; Pred. No. 0.00011;  
Matches      83; Conservative      0; Mismatches      19; Indels      0; Gaps      0;  
QY      1987 ACATCATTTGCTTTTAAATACATACCGTTTCTTTGCTTTTAAATAA 2046  
Db      2542 AGATTGTTTCTAAACAATAAGGCTTATTCTAAGTGTAAATAA 2601  
QY      2047 AAAAAA 2088  
Db      2602 AAAAAA 2643

RESULT 7  
US-09-095-443-1  
Sequence 1, Application US/09095443  
Patent No. 6342593  
GENERAL INFORMATION:  
APPLICANT: Plowman, Gregory  
APPLICANT: Peles, Elor  
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT  
TITLE OF INVENTION: OF ALP RELATED DISORDERS  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSES: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700

CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq for Windows 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/095,443  
FILING DATE: Herewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/049,477  
FILING DATE: June 12, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 235/055  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4456 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-095-443-1

Query Match      3.4%; Score 71.4; DB 3; Length 4456;  
Best Local Similarity      77.0%; Pred. No. 0.00014;  
Matches      87; Conservative      0; Mismatches      26; Indels      0; Gaps      0;  
QY      1976 CGATGATGTTTCATCATTTGCTTTTATACATACCGTTTCTTTGCTTTTAAAAA 2035  
Db      4337 CGACATTTTTCAGCTCTTTGCTTTGAAATATAAACCCCTGTTGTA 4396  
QY      2036 AAAAAA 2088  
Db      4397 AAAAAA 4449

RESULT 8  
US-09-845-917A-28/c  
Sequence 28, Application US/09845917A  
Patent No. 6653529  
GENERAL INFORMATION:  
APPLICANT: Bogaert, Thierry  
APPLICANT: Vandekerckhove, Joel  
TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH  
TITLE OF INVENTION: CONTROL CELL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND  
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING THEM AND THEIR  
TITLE OF INVENTION: USE IN THE CONTROL OF CELL BEHAVIOUR  
FILE REFERENCE: P/14-1  
CURRENT APPLICATION NUMBER: US/09/845,917A  
CURRENT FILING DATE: 2001-04-30  
NUMBER OF SEQ ID NOS: 58  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO: 28  
LENGTH: 10288  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (8456)  
OTHER INFORMATION: "N is A, C, G, or T"  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: artificial  
OTHER INFORMATION: plasmid

RESULT 10  
US-10-140-002-207  
; Sequence 207, Application US/10140002  
; Patent No. 6725730  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura

	Query Match	3.4%	Score 70.8	DB 3	Length 1569
	Best Local Similarity	44.2%	Pred. No. 0.00012		
	Matches 381	Conservative	Mismatches 477	Indels	Gaps 2
Qy	1231	GGGCTCTACTCAACTCGGTATTCTTAGGGTTACGTCGTTCTGTATCGAGGCCATGTGC	1290		
Db	178	GCGCCCTCATCGACGCGCGGAGCTGGGGTCTCTGTCGTGTATCGCCCGGTGATCGCC	237		
Qy	1291	CGGAAGGTCGGGCCGAGGGTGGTGTGGGTGACGAGCAACTTCATGTCTGTGCTGCGCATG	1350		





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; CURRENT APPLICATION NUMBER: US/09/554,337
; CURRENT FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/065,791
; PRIOR FILING DATE: 1997-11-14
; PRIOR APPLICATION NUMBER: PCT/CA98/01064
; PRIOR FILING DATE: 1998-11-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 8100
; TYPE: DNA
; ORGANISM: respiratory syncytial virus
US-09-554-337-4

Query Match          3.4%; Score 70.8; DB 4; Length 8100;
Best Local Similarity 67.8%; Pred. No. 0.00021;
Matches 99; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

Qy 1943 CGATCAATCAATGTGTAGTAGTACAACTAGACGATGATGTCACATCATTTGCTTTTA 2002
Db      |||||
Qy 7859 CAATAATTGGAAGCTTACATAAGCTTAATTCGACGATAATTTGGATTTTATTTT 7918
Db      |||||
Qy 2003 ATACATACCGTTTCTATTGCTTTTAAAAAIAAAAAAAAAAAAAAAAAAAAAAAAAA 2062
Db      |||||
Qy 7919 GCAATTGGTTTTTAATATTTCACAAAAAIAAAAAAAAAAAAAAAAAAAAAAAAAA 7978
Db      |||||
Qy 2063 AAAAAAAAAAAAAAAAAAAAAAAAAA 2088
Db 7979 AAAAAAAAAAAAAAAAAAAAAAAAAA 8004

RESULT 15
US-07-920-281C-1
; Sequence 1, Application US/07920281C
; Patent No. 5739026
; GENERAL INFORMATION:
; APPLICANT: Garoff, Henrik
; APPLICANT: Liljestrom, Peter
; TITLE OF INVENTION: DNA Expression Systems Based on
; TITLE OF INVENTION: Alphaviruses
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch
; STREET: P.O. Box 747
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/920,281C
; FILING DATE: 13-AUG-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy Jr., Gerald M.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 828-103P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-241-1300
; TELEFAX: 703-241-2848
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11517 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA (genomic)
; HYPOTHETICAL: NO
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; ANTI-SENSE: NO
; ORIGINAL SOURCE: Semliki Forest Virus
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..11517 /label= genome
; OTHER INFORMATION: /note= "Semliki Forest Virus complete nucleotide
; OTHER INFORMATION: sequence, presented as a cloned DNA sequence; see
; OTHER INFORMATION: Figure 5."
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 87..7379
; OTHER INFORMATION: /product= "SFV polyprotein"
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 7421..11179
; OTHER INFORMATION: /product= "SFV polyprotein"
US-07-920-281C-1

Query Match          3.4%; Score 70.8; DB 1; Length 11517;
Best Local Similarity 67.8%; Pred. No. 0.00024;
Matches 99; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

Qy 1943 CGATCAATCAATGTGTAGTAGTACAACTAGACGATGATGTCACATCATTTGCTTTTA 2002
Db 11362 CAATAATTGGAAGCTTACATAAGCTTAATTCGACGATAATTTGGATTTTATTTT 11421
Qy 2003 ATACATACCGTTTCTATTGCTTTTAAAAAIAAAAAAAAAAAAAAAAAAAAAAAAAA 2062
Db 11422 GCAATTGGTTTTTAATATTTCACAAAAAIAAAAAAAAAAAAAAAAAAAAAAAAAA 11481
Qy 2063 AAAAAAAAAAAAAAAAAAAAAAAAAA 2088
Db 11482 AAAAAAAAAAAAAAAAAAAAAAAAAA 11507

Search completed: November 7, 2004, 14:41:40
Job time : 188 secs
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1	1557	74.6	1557	15	US-10-409-701-18	Sequence 18, Appl
2	1472.8	70.5	1499	16	US-10-425-114-31902	Sequence 31902, A
3	1344.8	68.4	2248	18	US-10-425-115-342617	Sequence 142617, A
4	1302.4	62.4	2470	17	US-10-767-701-14354	Sequence 14354, A
5	1291.4	61.8	1372	16	US-10-425-114-35042	Sequence 35042, A
6	1052.2	50.4	2223	15	US-10-431-273-24	Sequence 24, Appl
7	1040.6	49.8	2092	15	US-10-431-273-22	Sequence 22, Appl
8	840.4	40.2	1600	15	US-10-431-273-23	Sequence 23, Appl
9	826.2	39.6	1831	15	US-10-310-154-359	Sequence 359, App
10	678.8	32.5	2235	18	US-10-739-930-4637	Sequence 4637, Ap
11	634.2	30.4	695	16	US-10-425-114-12513	Sequence 12513, A
12	586.6	28.1	1910	16	US-10-425-114-4380	Sequence 4380, Ap

QY 322 GCGGGGGGTCAGTACGGCTGGGGGCTGAGCTCTCCCTCTCACGCCCTACGTGACG 381  
Db 121 GCGGGGGGTCAGTACGGCTGGGGGCTGAGCTCTCCCTCTCACGCCCTACGTGACG 180  
QY 382 ACTCTGGGGTTTACATGCGCTCACTTCATTCAITGAGCTCTGCGGCCCTATTCCGGC 441  
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QY 442 TTAGTGGTCCACCGCTGCTGGCTGTACAGGACAGGTGTACATCAGATGGGGAGA 501  
Db 241 TTAGTGGTCCACCGCTGCTGGCTGTACAGGACAGGTGTACATCAGATGGGGAGA 300  
QY 502 CGAGGCGGTTTATCTCGACAGGGTGCATGCTCATCTGCGTTGCCGTCAITGTTGTCGA 561  
Db 301 CGAGGCGGTTTATCTCGACAGGGTGCATGCTCATCTGCGTTGCCGTCAITGTTGTCGA 360  
QY 562 TTCTGCTCAGACATCGAGCTGCTTAGGGGACAGAGGACACTGAGCCTCTACAC 621  
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QY 622 GGTCTCGTGGCAGCTCGATCGGTGACGTCTCTGGGGTTTGGCTCCTTGAATTCCTC 681  
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QY 682 ACAAACACTGTGACGGTCCAGACGTGCTATGATGGCTGATCTATGTGACCATCGG 741  
Db 481 ACAAACACTGTGACGGTCCAGACGTGCTATGATGGCTGATCTATGTGACCATCGG 540  
QY 742 CCAAGTGGGCTAACTCCATCTCTCTGTTCTGGATGGGCTGGGAAACATCTAGGCTAC 801  
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Db 601 TCTCTGCTCCAGACATGTCAGACAGTGGTTTCCCTTCTTAAACAGAGGCTGTC 660  
QY 862 TGTGAGGCTGTGCGAACCTGAAAGGTGCAITTTCTGTTGGGCGGTGGTCTTCTAGTCTG 921  
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QY 922 TGCCTGACGTAACCTGATCTTCCGACAGAGTGGCGGTACAGACGAGCAACCTC 981  
Db 721 TGCCTGACGTAACCTGATCTTCCGACAGAGTGGCGGTACAGACGAGCAACCTC 780  
QY 982 CCGACGACGAAGCGCGGCGGAGTTCGAGACTGAGCCTACCGGCGCACTTGCGGTGCTC 1041  
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QY 1102 TGGCTTTCTGTTTCCGTTTCTATCTCTACGACACCGACTGATGGGCGGAGATCTAC 1161  
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QY 1222 GCGGCTTCCGGCTGCTACTCAACTCGGTTATTCTAGGGTTTCACTGCTTCTCTGATCGAG 1281  
Db 1021 GCGGCTTCCGGCTGCTACTCAACTCGGTTATTCTAGGGTTTCACTGCTTCTCTGATCGAG 1080  
QY 1282 CCCATGTCCGAAAGGTGCGGCGGAGGTGCTGGGTGACGACAACTTCACTGGTCTGC 1341  
Db 1081 CCCATGTCCGAAAGGTGCGGCGGAGGTGCTGGGTGACGACAACTTCACTGGTCTGC 1140  
QY 1342 GTCCGATGGCGGCGCACCGGCTGATCAGCTTCTGGTCTGAGGACTACCAACGGGTAC 1401  
Db 1141 GTCCGATGGCGGCGCACCGGCTGATCAGCTTCTGGTCTGAGGACTACCAACGGGTAC 1200

## RESULT 2

US-10-425-114-31902  
; Sequence 31902, Application US/10425114  
; Publication No. US2004003488A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E.  
; APPLICANT: Tabaska, Jack E.  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 31902  
; LENGTH: 1499  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: UC-ZMFLB73232A01\_FLI  
US-10-425-114-31902

Query Match 70.5%; Score 1472.8; DB 16; Length 1499;

Best Local Similarity 99.5%; Pred. No. 3.1e-311;

Matches 1488; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 534 CATCTGCTGCTCCCTCATTTGTTGCGGATTTCTCGTACAGATCGGAGCTCTTAGGGGA 593  
Db 3 CGTGTGATATAGTCAATTTGTTGCGATTTCTGTACACATCGGAGCTCTTAGGGGA 62  
QY 594 CACGAAGAACATGACGCTCTACCAACGCTCTCTGTTGGCAGCTGCGATCGTACGT 653  
Db 63 CACGAAGAACATGACGCTCTACCAACGCTCTCTGTTGGCAGCTGCGATCGTACGT 122  
QY 654 TCTGGGTTTTGGCTCCTTGCATTTCTCCAAACACTGTGCGAGGTCACAGACGTGCTAT 713  
Db 123 TCTGGGTTTTGGCTCCTTGCATTTCTCCAAACACTGTGCGAGGTCACAGACGTGCTAT 182  
QY 714 GATGGCTGATCTATGTGACCATCATGGGCCAAGTGGGCTAACTCCATCTTCTGTTCTTG 773  
Db 183 GATGGCTGATCTATGTGACCATCATGGGCCAAGTGGGCTAACTCCATCTTCTGTTCTTG 242  
QY 774 GATGGCTGGAAACATCTTAGGCTACTCTCTGGCTCCAGCAAAATTGGCAAGTG 833  
Db 243 GATGGCTGGAAACATCTTAGGCTACTCTCTGGCTCCAGCAAAATTGGCAAGTG 302



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Db      814  GATGGCTGATCTGTGCGGTATCATATGGGCTTAGTGACGCAACTCAATCTTCCTGTTCTTG 873
Qy      774  GATGGCGTGGGAAACATCTTAGCTACTCTCTGGCTCCACGAAACAATTTGGCACAAAGTG 833
Db      874  GATGGCGTGGGAAACATCTTAGCTACTCTCTGGTTCACAAACAACATGGGCACAAAGTG 933
Qy      834  GTTTCCTCTCTTAAACGAGCGCTCTGTGAGGCGTGTGCGAACCTGGAAGGTGCATT 893
Db      934  GTTTCCTCTCTTAAACGAGCGTCTGTGAGGCGTGTGCGAACCTGGAAGGTGCATT 993
Qy      894  TCTGGTGGCGTGTGTTCTTAGTCTCTAGTCTGCTGACGTAACCTGATCTTCCCAAGGA 953
Db      994  TCTGGTGGCGTGTGTTCTTAGTCTCTAGTCTGCTGACTATAACCTGTTCTTCCCAAGGA 1053
Qy      954  GGTGCGGTACAGAGCGAACGAAACCTCCGACGACGAGCGCGGCGAGGTCCAGAC 1013
Db      1054  AGTGCCCTACAGAGGAAACCAAGAACCTCC---CCACAAAGGCAACCGCGAGGTCCAGAC 1110
Qy      1014  TGAGCTACCGGCGCACTTGGCGGTCTCAAGGGCTTCAAGGCTCTCCCGGATGCC 1073
Db      1111  TGAACCTTCCGCGCCACTCGCTGTGCTCAAGGGCTTCAAGGCTTCAAGGCTTCCCGATGCC 1170
Qy      1074  CTCCTGTCTCTCTGACTGCTGATCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1133
Db      1171  CTCCTGTCTCTCTGACTGCTGATCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1230
Qy      1134  CACGACTGATGGCGGAGATCTACACGCGGACCCCAAGGGAGCAACGCCAGAT 1193
Db      1231  CACGACTGATGGCGGAGATCTACACGCGGACCCCAAGGGAGCAACGCCAGAT 1290
Qy      1194  CTCGCGCTTCAACGAAGGTGTCCGAGTGGCGCTTCCGGCTGCTACTCAACTCGGTTAT 1253
Db      1291  CTCGCGCTTCAACGAAGGTGTCCGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1350
Qy      1254  TCTAGGTTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1313
Db      1351  TCTAGGTTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1410
Qy      1314  GTGGGTGACGACCAACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1373
Db      1411  GTGGGTGACGACCAACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1470
Qy      1374  CTGCTGCTGACGACCAACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1433
Db      1471  CTGCTGCTGACGACCAACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1530
Qy      1434  CAAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1493
Db      1531  CAAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1590
Qy      1494  CTTCCCGTTCGCGGTGACGCGGCGACTGCGGCGCAACCCGCGGCGCGGCGGCGGCGGCGGCTG 1553
Db      1591  CTTCCCGTTCGCGGTGACGCGGCGACTGCGGCGCAACCCGCGGCGCGGCGGCGGCGGCGGCTG 1650
Qy      1554  CACCGGCTCTCAACTCTCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1613
Db      1651  CACCGGCTCTCAACTCTCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1710
Qy      1614  CCGGTGGACGCGCTGTTTCCGGAAGGCAACATCCCGCGTTCGCGGTTCGCGGTTCGCGGTTCG 1673
Db      1711  CCGGTGGACGCGCTGTTTCCGGAAGGCAACATCCCGCGTTCGCGGTTCGCGGTTCGCGGTTCG 1770
Qy      1674  GCGCTCTGCGGCGGCTGCTGCGGCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1733
Db      1771  GCGCTCTGCGGCGGCTGCTGCGGCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1830
Qy      1734  CCGGCGCTGACGCGGCGGCGCACTGATCGAAACCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1793
Db      1831  CCGGCGCTGACGCGGCGGCGCACTGATCGAGCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1890
Qy      1794  AGCCCGGC 1801
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Db      1891  GGCACGGC 1898
RESULT 4
US-10-767-701-14354
; Sequence 14354, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 53128
; SEQ ID NO 14354
; LENGTH: 2470
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CJUS2418_1
US-10-767-701-14354
Query Match      62.4%; Score 1302.4; DB 17; Length 2470;
Best Local Similarity 87.5%; Pred. No. 5.8e-274;
Matches 1449; Conservative 0; Mismatches 201; Indels 6; Gaps 2;
Qy      132  CTAGTACTAGTAGGGCGGACCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 191
Db      290  CTAGTCTCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 349
Qy      192  TGTGCTGCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 248
Db      350  CGCGTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 409
Qy      249  CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 308
Db      410  CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 469
Qy      309  CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 368
Db      470  CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 529
Qy      369  GCGCTACGTGACAGCTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 428
Db      530  GCGCTACGTGACAGCTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 589
Qy      429  CCTATTGCGCGCTTAGTGGTCCAAACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 488
Db      590  TCTATTGCTGCTTAGTGGTTCACACCGTGGTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 649
Qy      489  GAGATGGGGGAGACGAGGCGCGCTTATCTGACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 548
Db      650  AAGATGGGGGAGACGAGGCGCGCTTATCTGACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 709
Qy      549  CATTTGTTGCGATTCTGCTGACAGATCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 608
Db      710  CATTTGTTGCGATTCTGCTGACAGATCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 769
Qy      609  GAGCCTCTACCAAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 668
Db      770  GAGTCTCTATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 829
Qy      669  CTTTGAATCTCCAAACACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 728
Db      830  CTTTGAATCTCCAAACACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 889
Qy      729  TGACCATCATGCGGCGCAAGTGGCGGCTAACTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 788
Db      890  CGGTCTCATGCGGCGCTAGTGGCAGTAACTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 949
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QY 817 AACAAATGGGACAAAGTGGTTTCCTTCTTAAACGAGCGCTGCTGTGAGGCGCTGTGG 876  
 Db 714 AACAAATGGGACAAAGTGGTTTCCTTCTTAAACGAGCGCTGCTGTGAGGCGCTGTGG 773  
 QY 877 AACCTGAAAGGTGCAATTTCTGGTGGCGGTGGTGTCTAGTCTGTGCTGAGCGGTAAAC 936  
 Db 774 AACCTGAAAGGTGCAATTTCTGGTGGCGGTGGTGTCTAGTCTGTGCTGAGCGGTAAAC 833  
 QY 937 CTGATCTTCCGCAAGAGGTGCCGTACAGAGCGAAGCAAGCACTCCCGACGACGAGGCC 996  
 Db 834 CTGATCTTCCGCAAGAGGTGCCGTACAGAGCGAAGCAAGCACTCCCGACGACGAGGCCA 893  
 QY 997 GCGCGAGGTGCGAGCTGAGCTTACCGGGCACTTCCGGTGTCTCAAGGGCTTCAAGGAC 1056  
 Db 894 GCGCGAGGTGCGAGCTGAGCTTACCGGGCACTTCCGGTGTCTCAAGGGCTTCAAGGAC 953  
 QY 1057 CTGCTCCCGGATGCCGTGCTCTCTGTGACTGCCATFCACTGGCTTTCTGTGGTTTC 1116  
 Db 954 CTGCTCCCGGATGCCGTGCTCTCTGTGACTGCCATFCACTGGCTTTCTGTGGTTTC 1013  
 QY 1117 CGGTTCATCTTACGACACGCTGATGGCGCGGAGATCTACACGCGGACCCCAAG 1176  
 Db 1014 CGGTTCATCTTACGACACGCTGATGGCGCGGAGATCTACACGCGGACCCCAAG 1073  
 QY 1177 GGGAGCAACGGCCAGATCTCGCGCTTCAACGAAAGGTGTCCGAGTGGCGGGTTCGGGCTG 1236  
 Db 1074 GGGAGCAACGGCCAGATCTCGCGCTTCAACGAAAGGTGTCCGAGTGGCGGGCTG 1133  
 QY 1237 CTACTCAACTGGTTATCTTAGGTTGATGCTCTCTGTGACTGAGCCCATGTGCGGGAAG 1296  
 Db 1134 CTACTCAACTGGTTATCTTAGGTTGATGCTCTCTGTGACTGAGCCCATGTGCGGGAAG 1193  
 QY 1297 GTGCGCGGAGGTGGTGGTGCAGAGCAACTTCATGGTCTCGCTGCGCATGGCGGCC 1356  
 Db 1194 GTGCGCGGAGGTGGTGGTGCAGAGCAACTTCATGGTCTCGCTGCGCATGGCGGCC 1253  
 QY 1357 ACCGCGGTGATGATCTTGTGCTGAGGACTACCAAGGAGTGTGAGGAGTGTGAGGAGCCATC 1416  
 Db 1254 ACCGCGGTGATGATCTTGTGCTGAGGACTACCAAGGAGTGTGAGGAGTGTGAGGAGCCATC 1313  
 QY 1417 ACCGCGAAGCGGACATCAAGCGCTGCTGCTGCTCTTTCGCTCTTTCGGGCTGCC 1475  
 Db 1314 ACCGCGAAGCGGACATCAAGCGCTGCTGCTGCTCTTTCGCTCTTTCGGGCTGCC 1372

RESULT 6

US-10-431-273-24  
 ; Sequence 24, Application US/10431273  
 ; Publication No. US20030237108A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Demmer, Jeroen  
 ; APPLICANT: Shenk, Michael Andrew  
 ; APPLICANT: Glenn, Matthew  
 ; APPLICANT: No. US20030237108A1riss, Michael Geoffrey  
 ; APPLICANT: Saulsbury, Keith Martin  
 ; APPLICANT: Hall, Claire  
 ; APPLICANT: Foster, Richard L. S.  
 ; TITLE OF INVENTION: Compositions isolated from forage  
 ; FILE OF INVENTION: Grasses and methods for their use.  
 ; FILE REFERENCE: 11000.10690  
 ; CURRENT APPLICATION NUMBER: US/10/431,273  
 ; CURRENT FILING DATE: 2003-05-06  
 ; NUMBER OF SEQ ID NOS: 92  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 24  
 ; LENGTH: 2223  
 ; TYPE: DNA  
 ; ORGANISM: Festuca arundinacea  
 US-10-431-273-24

Query Match 50.4%; Score 1052.2; DB 15; Length 2223;  
 Best Local Similarity 77.3%; Pred. No. 2.2e-219;  
 Matches 1303; Conservative 0; Mismatches 378; Indels 4; Gaps 2;

QY 1115 CGGTCCATCGATCCTAGTAGTAGTAGGGCGGACCGTCTCGTCTCGTGGTGGT 174  
 Db 169 CCTCTCTAGATCCTTGTGTGGCCGAAGTAATGATAGCGCAACGAGGTGATCATCTGTTCCG 228  
 QY 175 GACAGGTCCCGTACGTGTGTGTGCTGCCATAGTCTGTGGCGACGGCGGCGAGTCCGCGAG 234  
 Db 229 ACGAGTCTCCGCGCATG -GTGCGGGCGGCGCAACAGCGAGGTGGAGCTCTCCGTGGG 287  
 QY 235 CTGTCCGCGGGGTCCGCGGCGCGCGTGTGTGACACACGTGGCCCGATCAGGCTC 294  
 Db 288 GCGGTGTGCGGGCGGCGGCGGAGCGCTGTGTGAGCGCGCCCGTGTCCCATCAGGCTC 347  
 QY 295 GGGAGGCTCATCTCCCGCGCATGTGTCGCGCGCGGTGACGTACGGGTGGCGGCGCTGACG 354  
 Db 348 GGCAGGCTCTGCTTCCCGCGCATGGTCCGCGCGGTGACGTATGGATGGCGCTCCAG 407  
 QY 355 CTCTCCCTCTCAACGCGCTACGTGCGAGACTCTGGGCTTTTACATGCGCTCAGTTCATTC 414  
 Db 408 CTCTCCCTCTCAACGCGCTACGTGCGAGACTCTGGGACTTTTACATGCGCTCAGTTCATTC 467  
 QY 415 ATGTGCTCTGCGGCGCTTATGCGGCTTGTGTGTCACACCGCTGTGTGGCTGTACAGC 474  
 Db 468 ATGTGCTCTGCGGCGCTTATGCGGCTTGTGTGTCACACCGCTGTGTGGCTGTACAGC 527  
 QY 475 GACAGGTGTACATCGAGATGGGGGAGACGGAGCGGCTTTATCTGACAGGTGTGATGCTC 534  
 Db 528 GATAAGTGCACATCCAGATGGGAAGACGGAGCGGCTTTATATACAGGATGTGTGCTC 587  
 QY 535 ATCTGGGTGCGCTCATTTGTGCGATTTCTGACATCGGAGCTGCTTAGGGGAC 594  
 Db 588 ATATGATGCTGCTTGTGATTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 647  
 QY 595 ACGAAGGAACACTGACGCTCTTACACGCTCTCTGCTGGCACCGTGTCAATTTGTGTGCTG 654  
 Db 648 ACCAAGGAAGAGTGCAGTCTTACCATGCTCTGCTGGCACCGTGTCAATTTGTGTGCTG 707  
 QY 655 CTGGGGTTTTGGCTCTGCTTCTTCCAAACACTGTGAGGCTTCAGACGCTGCTATG 714  
 Db 708 CTGGAATCTGGCTTCTTGTGCTTCTTCCAACTACTGTGCAAGGTTCAGCTGCTGCTGCT 767  
 QY 715 ATGGCTGATCTATGTGACCATCATGGGCAAGTGGCTAACTGCTCTTCTGTTCTTGG 774  
 Db 768 ATGGCTGATTTGTGAGCAAGATGTGACCCAGTGTGCAATTTCAATTTCTGTTCTTGG 827  
 QY 775 ATGGCGCTGGGAAACATCCTAGGCTACTCTTGTGCTCCAGCAATTTGCAAGTGG 834  
 Db 828 ATGGCGCTAGGAAATATCCTAGGCTACTCTTGTGCTCCAGCAATTTGCAAGTGG 887  
 QY 835 TTTTCCCTTCTTAAACGAGCGCTGCTGTGAGGCTGTGGCACTTGAAGGTGCTATTT 894  
 Db 888 TTTTCCCTTCTTGGCAAGAGCTGCTGTGAGCTTGGCAATTTGAAGGCGCTTTT 947  
 QY 895 CTGTGGCGGTGGTCTTCTAGTCTGTGCTGAGCGTAACTGCTGATCTTCCGCAAGGAG 954  
 Db 948 CTGTGGCGGTGGTCTTCTAGTCTGTGCTGAGTAACTGCTGATCTTCCGCAAGGAG 1007  
 QY 955 GTGCGGTACAGAGCGAAACGAGAACCTCCGCGAGCGGCGGCGGAGTCCAGACT 1014  
 Db 1008 GTACCATACAAACGAAATTTGCAAGGCTTCCAGGCTTCCAGGCTTCCGCAAGTGG 1064  
 QY 1015 GAGCTTACCGGGCCACTTCCGCTGTCTCAAGGCTTCAAGGACCTGCTTCCCGGATGCGC 1074  
 Db 1065 GAACCTAGTGGCGCGCTTGGGCTTCCAGGCTTCCAGGCTTCCGCTTCCGCAAGTGG 1124  
 QY 1075 TCGTGTCTCTGCTGACTGAGCTGCTTCTGCTGCTTCTGCTGCTTCTCTTCTAGCAG 1134  
 Db 1125 TCGGTGCTCTTGTAACTGGGCTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1184  
 QY 1135 ACCGACTGATGGCGGGGAGATCTTACACGCGGCAACCCCAAGGGGAGCAACGCCAGATC 1194  
 Db 1185 ACCGACTGATGGGTGCTGAGATTTTACACGCTGACCCCAAGGGGACCCCGAGTGGGCC 1244



1273	QY	CTGATCGAGCCCATGTGCCGAAAGTTCGGCCGAGAGGTGTGTGGTGACGAGCAATTC	1332
1306	DB	CTGATCGAGCCGATGTCAAGCGGCTAGGCCGAGAGGTGTGTGGTGTCGAGCAATTC	1365
1333	QY	ATGGTCTTCGCTCGCCATGCGGGCCACCGCGCTGATCAGCTTCTGGTCGCTCAGGGACTAC	1392
1366	DB	CTCGTCTGCAATCGCTATGGTGCACCGCCATCATCAGCTGGTGGTCTACCAAGGAATTC	1425
1393	QY	CAGGGTAGCTGAGAGACGCATACACCGGAAACGCCAGACATCAAGGCCGTCTGCCTCGTC	1452
1426	DB	CATGAGTACGTTGAGCATGCGATTACCGCCAGCAAGGACATCAAAATCGTATGCATGGCC	1485
1453	QY	CTCTTTGGCCCTTCTGGCGCTCCCTCTCGCCATCCTGTACAGCGTCCCGTTTCGGGTGACG	1512
1486	DB	CTCTTGCATCTCTGGAGTGCCTCTCGCCATCTCTGTACAGCGTCCCTTTGGGTGACG	1545
1513	QY	GCCAGCTGGCGGCACCCGGGGGGGGGACAGGGGTGTGTACACGGCGTCTCTCAACATC	1572
1546	DB	GCGCAGTTGGCGCAAGCAAGGAGGGCGGCAAGGGCTGTGTACACGGCGTCTGTAATATC	1605
1573	QY	TCCATCGTCAATCCTCAGGTGATCATCGCGCTGGCGCCGGCCGCTGGGACGCGCTGTTC	1632
1606	DB	TCCATCGTCAATCCCAAGGTGATCATCGCGTGGGGCGGGGCGTGGGACCAAGCTGTTTC	1665
1633	QY	GGGAAGGCAACATCCCGCGCTTGGCGGTCCGCTCGGCCCTTCGCCCTCGTCGGCGGCTC	1692
1666	DB	GGGAAGGCAACATCCCGCGCTTGGCGCGGCCCTTCGCCCTTCGCGCTCATCGCGCGCATC	1725
1693	QY	GTGGGGGTGTTCTGTGTGCCCAAGATCTCAAGGCCAGTTCGCGGCCGCTCAGCGGGGC	1752
1726	DB	GTGGCAATATCTGTGCCCAAGATCTCAGAGCGCTCTGTTCCGGGCCGTGACACCGGC	1785
1753	QY	GGCACTGATCGAAACCGCGCGGGCGGCCCGCCGCAACGACCGG	1799
1786	DB	GGTCACTGACCGGTCGGGGCGCTGCTGAGCGCGCGGAAGCTCG	1832

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RESULT 8
US-10-431-273-23
; Sequence 23, Application US/10431273
; Publication No. US20030237108A1
; GENERAL INFORMATION:
; APPLICANT: Demmer, Jeroen
; APPLICANT: Shenk, Michael Andrew
; APPLICANT: Glenn, Matthew
; APPLICANT: No. US20030237108A1, Michael Geoffrey
; APPLICANT: Saulsbury, Keith Martin
; APPLICANT: Hall, Claire
; APPLICANT: Forster, Richard L. S.
; TITLE OF INVENTION: Compositions isolated from forage
; TITLE OF INVENTION: Grasses and methods for their use.
; FILE REFERENCE: 11000.1069U
; CURRENT APPLICATION NUMBER: US/10/431,273
; CURRENT FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 1600
; TYPE: DNA
; ORGANISM: Festuca arundinacea
US-10-431-273-23

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	Query Match	40.2%	Score 840.4;	DB 15;	Length 1600;
	Best Local Similarity	79.5%;	Pred. No. 3.1e-173;		
	Matches 1007;	Conservative	0;	Mismatches 256;	Indels 3; Gaps 1;
QY	534	CATCTCGTTGCCGTCAATGTTCTCGAATTCTCGT	CAGACATCGGAGCTGCTCTACGGGA	593	
DB	2	CATCTCGTTGCTGTTGTGTGTCGTCTCGGTCGACATGGAGCTGCTCTGGGTGA	61		
QY	594	CACGAAGGAACACTGGACGCTCTTACACGCTCTCTGTTCGACGCTGCATCGTGACGT	653		
DB	62	TAGCAAGGAAGAGTGCAGTCTCTTACCATGTCTCTCGTGTGCACGCTGCAAATCTGTATGT	121		

Qy	654	CTGGGGTTTGGCTCTCTTGACATCTTCCAAACAACATGTGCAGGGTCCAGCAGTGTCTAT	713
Db	122	GCTTGGATTCTGGCTTCTTGACATCTTCCAAACAATCTGTGCAAGGTCCAGCTCGTGCTCT	181
Qy	714	GATGGCTGATCTATGTGACCATCATGGGCCAAGTGGGGCTAACTCCATCTTCTGTGTTCTTG	773
Db	182	GATGGCTGATTGTCAAGCAAGTATGGACCAGTGTGCATAATCTTCTGTGTTCTTG	241
Qy	774	GATGGCGCTCGGAAAACATCTCTAGGCTACTCTCTGGCTCCACGAAACAATTTGGCACAAGTG	833
Db	242	GATGGCGCTAGGAAAATATCTTAGGGTACTCTCTGGTTCCACAGATAAGTGGCACAAGTG	301
Qy	834	GTTTCCCTTCTTAAACAGACGCGCTGCTGTGAGGCGTGTGCGAACTGTAAGAGTGCATT	893
Db	302	GTTTCCCTTCTTCCGACAAGAGCGCTGTGTGAAGCTTTCGCAAAATTTGAAGCGCGTTT	361
Qy	894	TCGTGTGGCGGTGTGTTCTCTAGTCTCTGTGCCCTGACGGTAACCTGATCTTCCCAAGGA	953
Db	362	TCGTGTGGCGTGTCTGTCTCTGTGCTTCTGTGTTGTTGTTGATAACTCTGATCTTCCCAAGGA	421
Qy	954	GGTGGCGGTACAGAGCGAAACGAGAACTCCCGACGACGAAAGCGCGGGAGTCCAGAC	1013
Db	422	GGTACCATAACAACGAATTGCACCCCTCC--CAACAAAGGCAAAATGGTCAGTTGAAGT	478
Qy	1014	TGAGCTACTCGGGCCACTTGGCGTGTCTAAGGCTTCAAGGACCTGGCTCCCGGATGCC	1073
Db	479	TGAACCTAGTGGCCCGCTTGGCGTGTTCGAAGCTTTCAGAACTTGGCTTCGGAAATGCC	538
Qy	1074	GTCCGTGCTCTCTGACTGCCATCACTCGGCTTTCGTGGTTCCCGCTTCATCCTCTACCA	1133
Db	539	ATCGGTGCTCTGTAACTGGCTCACTGGCTGCTCTGGTCCCGTTCATCCTCTACGA	598
Qy	1134	CACCGACTGATGGCGCGGAGATCTACACGGCGACCCCAAGGGAGACACGCCAGAT	1193
Db	599	CACCGACTGATGGGTGCTGAGATTTACACGGTGAACCCCAAGGGACCCCGACTCAGGC	658
Qy	1194	CTCGGGTTCAACGAAGGTGTCCAGTTCGGCGGTTTCGGGCTGCTACTCAACTCGGTTAT	1253
Db	659	CTCGGCTTCCAGACGGTGTCAAGGCTGGCGGTTTCGGACTGCTACTCAACTCGATCAT	718
Qy	1254	TCTAGGGTTCAGTCTGTTCTGTATCGAGCCATGTGTCGGGAAGTTCGGCCGAGGGTGT	1313
Db	719	CTTGGGGTTTCACTCTTCTGTATCGAGCCGATGTGCAAGCGGCTGGGCCGAGGGTGT	778
Qy	1314	GTGGGTGACGAGCAACTTTCATGCTCTGCGTCGCCATGGCGGCCACCGCGCTGATCAGCTT	1373
Db	779	GTGGGTGTCAGCAACCTCTCTGCTGTGCATGCGCATGGCGGCCACCGCCATCATCAGCTG	838
Qy	1374	CTGGTCTCAGGACTACACGGTATCGTGAGGACGCATCACCGNAAACCCAGCAT	1433
Db	839	GTGGTCTACCAAGGAATTCATGATGCTGACGATGCGCATGCCATCACCGCAGCAAGACAT	898
Qy	1434	CAAGGCGCTGTGCTCGTCTCTTCGCCCTTCCTGGGCGTCCCTCTCGCCATCTCTACAG	1493
Db	899	CAAGATCGATGATCATGGTCTCTTCGCAATCTCTCGAGTGCCTCTCGCCATCTCTGATACAG	958
Qy	1494	CGTCCGTTTCGGGTGACGGCGCAGCTGGGGCCACCCGGGGCGGGCAGGGGCTGTG	1553
Db	959	CGTTCCTTTCGGGTGACGGCGAGTTGGCGGCAACAAAGAGGCGGGCCAGGGGTGTG	1018
Qy	1554	CACGGCGTCTCAACATCTCATCTCATCCCTCAGGTGATCATCGCGCTGGGCGCCGG	1613
Db	1019	CACGGCGTCTGAACATCTCCATCTCATCTCCACAAGTGATCATCGCGCTGGGGCGGG	1078
Qy	1614	CCGTTGGGACGCGCTGTTGGGAGGGCAACATCCCGGCTTCGGGCTCGCGTTCGCGCTT	1673
Db	1079	GCCGTGGGACCAAGCTGTTCGGGAGGGCAACATCCCGGCTTTCGCGCGGCTTCCGCCTT	1138
Qy	1674	CGCCCTCTGTCGGCGGCTGTGGGCGTGTCTCTGTGCCCAAGATCTCAAGCGCCAGTT	1733
Db	1139	CGGCTCATCGGCGGATCGTGGGCAATTCCTGCTGCCAAGATCTCAGGCACTCGTT	1198





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QY 1598 TCGCGTGGGCGCGCCCGCTGGAGCGCTGTTGGGAAGGCAACATCCCGGGTTCG 1657
Db 1767 TCGCGTGGGCGCGCGCGCTGGAGAGCTGTTGGCAAGGCAACATCCCGGGTTCG 1826
QY 1658 GCGTCCGCTGGCGCTTTCGCCCTCGTTCGGCGGCGTGTGGCGGTTCCTGCTGCCAAGA 1717
Db 1827 GCATGCGCTTCGCGCTTCGCGCTCATCGGGGATCGTCGCGCATATTCCTGCTGCCAAGA 1886
QY 1718 TCTCCAAGCGCCAGTTCCCGCGCGTTCAGCGCGGCGCCACTGATC 1763
Db 1887 TCTCCAAGCGCCAGTTCCCGCGCGTTCGCGCGCGTTCGCTGACTGAGC 1932

RESULT 11
US-10-425-114-12513
; Sequence 12513, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 12513
; LENGTH: 695
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 701180736_FLI
US-10-425-114-12513

Query Match 30.4%; Score 634.2; DB 16; Length 695;
Best Local Similarity 94.5%; Pred. No. 2.2e-128;
Matches 657; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 1069 ATGCGCTCGGTCTCTGCTGACTGCATCACTGGCTTGTGTTGCTCCGTTCACTCTC 1128
Db 1 ATGCGGTCTGCTGCTCTCTGCTGACTCACTGCTCTGTTGTTCCGTTTCACTCTC 60
QY 1129 TACGACACCGACTGGATGGCGCGTGGAGATCTTACCACGGCGACCCCAAGGGAGCAACGCC 1189
Db 61 TACGACACCGACTGGATGGCGCGTGGAGATCTTACCACGGCGACCCCAAGGGTACCAACGCT 120
QY 1189 CAGATCTCGCGTTCAACGAAGGTTCGAGTCGGCGGCTTCGGGCTGCTACTCACTCG 1248
Db 121 CAGATCTCGCGTTTCACGAAGGCTCAGAGTAGGCTGCTTCGGGCTGCTCAACTCG 180
QY 1249 GTTATTCTAGGGTTTCAGCTCGTTCTCTGATCGAGCCCATGTGCCGAAGCTCGGGCGAGG 1308
Db 181 ATCATTTCTAGGATTCAGCTCGTTCTCTGATCGAGCCCATGTGCCGAAGTGGGCGGAGG 240
QY 1309 GTGGTGTGGGTGACGAGCACTTCATGTTCTCGTTCGCCATGTGGCGGCCACCGCGCTGATC 1368
Db 241 GTGGTGTGGGTGACGAGCACTTCATGTTCTCGTTCGCCATGTGGCGGCCACCGCGCTGATC 300
QY 1369 AGCTTCTGTGCTCAGGAGCTTACCACGGGTACGTGCGAGGCGCCATCACCGCAACGCC 1428
Db 301 AGCTTCTGTGCTCAGGAGCTTACCACGGGTACGTGCGAGGCGCCATCACCGCGAGCAGC 360
QY 1429 AGCATCAAGCGCTGTGCTCTGCTCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCT 1498
Db 361 AGCATCAAGCGCTGTGCTCTGCTCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCT 420
QY 1489 TACAGTCCCGTTCGGGTGACGGCGAGCTGGCGGCCACCCGGGCGGGCGAGGGG 1548
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Db 421 TACAGGTCCTCGTTCGGGTGACGGCGAGCTGCGCGCACGAAGGGCGGGCGGCGAGGG 480
QY 1549 CTGTGCAACCGCGCTCTCAACATCTCCATCGTATCCTCAGGTGATCATCGCCTGGGC 1608
Db 481 CTGTGCAACCGCGCTCTCAACATCTCCATCGTATCCTCAGGTGATCATCGCCTGGGC 540
QY 1609 GCCGGCCCGTGGGACGGCGCTGTTCCGGAAGGGCAACATCCCGGCTTCGGGCTCGCGTCG 1668
Db 541 GCGGGCCCGTGGGACGGCGCTGTTCCGGAAGGGCAACATCCCGGCTTCGGGCTCGCGTCG 600
QY 1669 GCCTTGGCCCTCGTGGCGGGCGTGTGGGCGTGTTCCTGCTGCCAAGATCTCCAAAGGC 1728
Db 601 GGGTTCGCCCTCATCGCGCGCGTGTGGGCGTGTTCCTGCTGCCAAGATCTCCAAAGGC 660
QY 1729 CAGTTCCGGCGCTCAGCGGGCGGCGCACTGATC 1763
Db 661 CAGTTCCGGCGCTCAGCGGGCGGCGCACTGATC 695

RESULT 12
US-10-425-114-4380
; Sequence 4380, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 4380
; LENGTH: 1910
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700355830_FLI
US-10-425-114-4380

Query Match 28.1%; Score 586.6; DB 16; Length 1910;
Best Local Similarity 63.8%; Pred. No. 8.2e-118;
Matches 952; Conservative 0; Mismatches 514; Indels 27; Gaps 3;

QY 279 GGGCCCGATCAGCTCGGGAGGCTCATCTTCGCGGCGATGTCGCGGGCGGTGCACTA 398
Db 115 GGGCCCGATCAGCTCGGGAGTCTGTCGGCTCTTCTTGGCTGATGTTCTCGGGCGATCCAGTA 174
QY 339 CGGCTGGCGCGTGCAGCTCTCCCTCTCAGCCCTACGTGCAAGCTCTGGGGTTCACA 398
Db 175 CGGCTGGCGCGTGCAGCTCTCCCTCTCAGCTCTCTCGCTCTCTCAGACTCTTGGGATCTCGCA 234
QY 399 TGGCTCACTTCTTATGCTGCTCTGCGGCTCTGCGGCTCTTTCGGGCTAGTGTCCACCGCT 458
Db 235 CAGTAGTGTCTCTGATCTGATCTGCGGCTCTGCGGCTCTATCGCGGATTTGTGTGCAACCCAT 294
QY 459 GGTGGCTGTACAGCGACAGGTGTATCATCGAGATGGGGAGACGGAGCGCGTTATCTCT 518
Db 295 CGTGGGCTCTACAGCGACCGGTGACCTCGAAGATGGGCGGAGGAGGCGCTTCTATCTCT 354
QY 519 GACAGGTGATGCTCATCTGCTTGGCGTATGTTGTCGATTTCTGTCAGACATCGG 578
Db 355 CGCGGGATGATCATCATCTGCTCTCTGTTTGGTATCGGGTCTTCGCGGACATCGG 414
QY 579 AGCTGCTCTTAGGGGACACGAAGAACTACACGCTCTACACGCTCTCTGTTGGCAGCGC 638
Db 415 GCGGCGCTCTCGGACACGACGAGGACTGACACGCTTACCGGCTCCGCTGGTCCGC 474
QY 639 TGGATCGTGTAGCTTCGGGGTTCGCTTCCTTGAATTCCTTCCAAACACTGTGAGGG 698
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475	Db	CGCGCGCGTCTACATTTGCGGATTTTGGTTCCCTTGACTTCGCCAACACACGTGACAGG	534
699	Qy	TCAGACACGTGCTATGATGCTGATCT--ATGTGACCATCATGGGCCCAAGTGGCGCTAA	755
535	Db	ACGGCTCGCGGATGATGCGGACCTGGCAGCTGGACAGCAGCGGCCCAAGTTGGCCA	594
756	Qy	CTCCATCTTCTGTTCTTGGATGGCGCTGGGAAACATCCTAGGTACTCTCTTGCTCCAC	815
595	Db	GGCGATCTTCTCCCTGTGGATGGCCCTCGGCAGCGTCTCGGATACTGTTCGGCGGCAA	654
816	Qy	GAACAAATTGCACAAGTGGTTTCCCTTCCTTAAACGAGCGCCTGCTGTGAGGCCTGTGC	875
655	Db	CGCGAATGACACACTGGTCTCCTTGGCTCAAAACCGCGGTGCTTCGATGGTGGC	714
876	Qy	GAACCTGAAAGTGCATTCTTGGTGGCGGTGGTGTCTCTAGTCTGTGCTGACGGTAAC	935
715	Db	CAACCTCAAGGGCGCTTCTTGACTGGGTGGTCTCTATTATAATCAGCATGCTGTCCAC	774
936	Qy	CCTGATCTTCGCCAAGAGAGTGCCTGTACAGCGAAAGCCTCCGACGACGAAGC	995
775	Db	CTTGTGGCTCGCGGCGAGAGGG-----CTCGACAGGAAG	813
996	Qy	CGCGGGCGAGTCCAGACTGAGCTACCGGGCCACTTCCGCTGCTCAAGGCTTCAAGGA	1055
814	Db	CTTCGACACCTCGCGCGCGCGTCTCGCGTTCATGGATCTCTTCAAGACCCTCAAGAA	873
1056	Qy	CCTGCCTCCGGGATGCCGTTCGTGCTCTCTGCTGACGTCCATCCTCTGGCTTTCGTGTT	1115
874	Db	GCTTCCGCTCCCATGTTTCAGCGTGTCTCGCGCTCAGCGCGTCACATSGGCTCTGTTGTT	933
1116	Qy	CCGTTTCATCTCTACGACACCGACTCGATGGGCGGAGATCTACACACGGCAGCCCAA	1175
934	Db	CCCCCTTCTTCAGTACAAACCGACTGATGGCCCGGAGATCTTCCACGGCAGCGCA	993
1176	Qy	GGGAGCAACGCCAGATCTGGCGTTTCAAGAGGTGTCCGAGTCCGCGGTTCGGGCT	1235
994	Db	GGGCGCGGGGAAAGCGGACCTGTACGAAGCGCGGCTCCGCGAGGCGCATTCGGCT	1053
1236	Qy	GCTACTCAACTCGTATTCTAGGGTTACGTCGTTCTCATCGAGCCCATGTGCCGAA	1295
1054	Db	CCTATTCTGCTCGTCCGCTCGGTGTCACTCTCTTTCATCCCAGGCTGTGCCGAA	1113
1296	Qy	GGTCCGCCAGGGTGGTGGGTGACGAGCAACTTCATGCTGTGCTGCCCATGGCGC	1355
1114	Db	GCTCACGTCGCGGTCTGTCGTCGGTCAGCAGCCTGATGGTGTCTGCTCATGACGCG	1173
1356	Qy	CACCGCGCTGATCAGCTTCTGTTCTGCTCAGGACTACACGGGTACGTGAGGACGCCAT	1415
1174	Db	CATGGTCTCTCGGATGCTTCATGAGGGCTACAGGCCCTCGCTCGCGGCTCTCT	1233
1416	Qy	CACCGCAAGCCGACGA--TCAGGCGCTGTGCTCTCTCTTCGCCCTTCTGGGCGT	1472
1234	Db	CTCTGGCCCCGACACCTCGTTCAAGGCGGCGCCCTCGCATCTTCGCTCATCGCAT	1293
1473	Qy	CCCTCTCGCCATCTGTACAGCTCCGTTCTCGGGTGAAGGCGAGCTGGGGCCACCG	1532
1294	Db	CCCTCAGCGCTGCTCTACAGCTGCTTGGCGCGTGGCGCTCTGAGGTGCCACCGAGA	1353
1533	Qy	GGGCGGGCGGAGGGGTGTGCACCGCGCTCCTCAACATCTCAATCGTCTCACTCAGGT	1592
1354	Db	CGCGGTGTGTAAGTCTACCATTGGGTCTCAATGTCATCTCTTCCACAGCT	1413
1593	Qy	GATCATCGCGCTGGGCGCGGCCGTGGGACGCGCTGTCGGGAAGGGCAACATCCGCG	1652
1414	Db	GGTATCGCGCTGGGCGAGGCCCATTCGAGCGGCGCTTCAACAAGGAAGAACCCCGCG	1473
1653	Qy	GTTCCGGGCTCGGTCGCGCTTCCGCCCTCGCTGGGGGGTGTGGTGGCGTGTCTCTGCTGC	1712
1474	Db	CTTCGGCATGGCGCGCTTTCGCCCTTATCTGGCGGCTCTGGCGCTCATCTCTCTCC	1533
1713	Qy	CAAGATCTCAAGCCAGTTTCGGGCGCTCAGCGCGGGCGGCATCTGATGA	1765

Db 1534 AAGACGAGAGGGCTCTCCAAAGCCACCGTCAATGCGCGGCACCTGATCTA 1586

RESULT 13

US-10-425-115-120168

; Sequence 120168, Application US/10425115

; Publication No. US20040214272A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants

; FILE REFERENCE: 38-211532221B

; CURRENT APPLICATION NUMBER: US/10/425,115

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 369326

; SEQ ID NO 120168

; LENGTH: 2262

; TYPE: DNA

; ORGANISM: Zea mays

; FEATURE:

; OTHER INFORMATION: Clone ID: MET4577\_41077C.1

US-10-425-115-120168

Query Match 28.1%; Score 586.6; DB 18; Length 2262;

Best Local Similarity 63.8%; Pred. No. 8.7e-118;

Matches 952; Conservative 0; Mismatches 514; Indels 27; Gaps 3;

QY 279 GCGCCCGATCAGCCTCGGAGGCTCATCTCGCGGCATCGTCCCGCGCGGTGCAGTA 338

Db 314 GCGCGCGATAGCATCGTCGCGCTCTTCTGGCTGCATGCTCTCGCGGCATCCAGTA 373

QY 339 CGGCTGGGCGTGAGCTCCCTCCTCAGCCCTACGTACAGACTCTGGGGTTTCA 398

Db 374 CGGCTGGGCGTGAGCTCTCCCTCCTCTGCCCCACTCTCAGACTCTTGGGATCTCGA 433

QY 399 TCGCGTCACTTCATTCATGTGGCTCTCGGCGCCTATTGCGGGCTTAGTGGTCCAAACCGT 458

Db 434 CAGCTACGTGTCCTGCATGATGATCTCGGCGCTATCGCGGATTGTGGTGCACCCAT 493

QY 459 GGTTCGCTGTACAGCGACAGTGTACATCGAGATGGGAGACGAGCCGTTTATCCT 518

Db 494 CGTGGGCTACTACAGCAGCGGTGCACCTCGAAGATGGGCGGAGGAGCCCTTCACTC 553

QY 519 GACAGGGTGCACTCACTCGCTGCGGTTCGCTCACTGTTGTCGGATTCTCGTCAACATCGG 578

Db 554 CGGGGATGCATCATCATCTGCTCTGTGTTGGTGATCGGTTCTCGCGGACATCGG 613

QY 579 AGCTGCTTAGGGGACAGAAAGAACTAGAGCCTCTACAGGTCCTCGTTGGCACCG 638

Db 614 GGGCGGCTCTCGCGACACAAAGAGCATCGCAGCACGTTACCGGGCTCCGCTGTGGTCCG 673

QY 639 TCGATCTGTGACGTTCTGGGGTTTGGCTCCTTGACTTCTCAAACAACTGTGACGG 698

Db 674 CGCGCGGCTTACATGTTCGATTTGGTTCCTTGACTTCGCCAAACAACGGTACAGG 733

QY 699 TCCAGCAGTGTATGATGGTGTACTT---ATGTGACCATCATGGGCCAAGTGGGCTAA 755

Db 734 ACCGGCTCGCGGATGATGGCCGACCTGGCAGCTGGACAGCAGCGGCCCAACGTTGGCA 793

QY 756 CTCATCTCTGTTCTTCGATGGCGCTGGGAAACATCCTAGGCTACTCTCTGGCTCCAC 815

Db 794 GCGGATCTTCTCCCTGTGTGATGGCCCTCGCAGCGGTCTCGGATATCTTGTCCGCGCCA 853

QY 816 GAACAATTGGCAAGTGGTTTCCCTTTCCTTAAACGAGCGCCTGTGTGAGGCTGTGC 875

Db 854 CGCGAAATGGCAGCACTGGCTCCCTTGGCTCAAAACCGCGCGCTGTGGGATGCGTGC 913

QY 876 GAACTGAAGGTGATTTCTGGTGGCGGTGGTTCCTAGTCTCTGTGCTGACGCTAAC 935

Db 914 CAACCTCAAGGGCGCTTCTTGACTGGGGTGGTCTCTCATTAATCAGCATGTGTGTCAC 973

Qy	936	CCTGATCTTCCGCAAGGAGGTCCGTACAGACGAA	CGAGAACTCCGACGACGAAGGC	9395	
Db	974	CTTGTGGCTCCCGCGGAGGAGCG- - - - -	CTCGACAGGAAAG	1012	
Qy	996	CGCGGGGAGTTCGAGACTGAGCCCTACCGGGCCACTTGC	CGTGTCAAGGCTTCAAGGA	1055	
Db	1013	CGTCGACACCTCCGGCGCGGTCTCGCGTTCATGGATCTCTT	CAAGACCTCAAGAA	1072	
Qy	1056	CTGCTCCCGGATGCGGTCCGTCTCTGTGACTGCCATCACT	TGGCTTCTGCTGGTT	1115	
Db	1073	GCTTCCGGCTCCCATGTTTCAGCTGTCTCGCGTCA	CGGCGGTCACTGGCTCTGCTGGTT	1132	
Qy	1116	CCCGTTCACTCTACGACACCGACTGGATCGCGCGGAGAT	TACACA	CGCGACCCCAA	1175
Db	1133	CCCCTTCTTCAGTACAACCGACTGGATGGCGGGAGATCTT	CCACGGGAGCCCA	1192	
Qy	1176	GGGAGACACCGCCAGATCTCGGGTTCACAGAA	GGTGTCCGATCGCGCGGTTT	CGGCGTTCGGGCT	1235
Db	1193	GGGCGCGGGCGAAAGGCGGACCTGTACGAAGCCGGGT	CCGCGAGGCGGCATTCGGCT	1252	
Qy	1236	GCTACTCAACTCGGTATTCTAGGGTTACAGTCTGCTT	CTGATCGAGCCCATGTGCCGAA	1295	
Db	1253	CCATTCTGCTCGTGGCGTCTGGTGTACCTCTTCTT	CATCCGAGGCTGTGCCGAA	1312	
Qy	1296	GGTCGGGCGAGGTGGTGTGGGTGA	CGAGCACTTCATGCTTGCCTGCCCATGGCGGC	1355	
Db	1313	GCTCACGTCCGGGTCTGCTGCTCGTCAGCAGCTGAT	GGTGTCTGCTCATGACGC	1372	
Qy	1356	CACCGCTGATACGCTCTGGTCGCTCAGGACTACA	CGGGTACGTGCAGACGCAT	1415	
Db	1373	CATGGTCGCTCGGATGGTCTCCATGAAGGGTAC	AGGCCCTCGGTGCGCGGCTCCCT	1432	
Qy	1416	CACCGCAACCCAGCA- - - TCAAGCGCTTGCCT	CGTCTCTTCCTCCCTTCCTGGCGGT	1472	
Db	1433	CTCTGGCCCCACCACTCGTTTCAAGGCGGGCGCT	CGCCATCTTCGCGTCTATCGGCAT	1492	
Qy	1473	CCCTCTCGCATCTGTACAGCTCCGCTTCGCGGT	GACGCGCAGCTGGCGCCACCG	1532	
Db	1493	CCCTCAGCCGCTGTCTACAGCTGCTTGGCGCGT	GGCGTCTGAGGTGTCCACCGAGGA	1552	
Qy	1533	GGCGGGGGCAGGGGTGTGCACCGGCGTCTCAAC	ATTCATCTCATCTCCCTCAGGT	1592	
Db	1553	CGGCGGTGTCAGGTCTACCATTTGGGTCTCTCAA	CATTGCAATCTCTCTTCCACAGCT	1612	
Qy	1593	GATCATCGCGTGGGCGCGGCCGTCGGAC	CGCGCTGTTCCGGAAGGCGCAATCCCGGC	1652	
Db	1613	GGTGATCGCGTGGGCGAGGCCCCATCGAC	GGCGCCTTCGACAAAGAAACACCCCGGC	1672	
Qy	1653	GTTCCGGGTCTGCGCTTCGCGCTCTCGCGGGCGT	CGTGGCGGTGTTCTGCTGTGCC	1712	
Db	1673	CTTCGGCATCGCGCGGCTTCGCGCTTATCTGCGCGT	CTGTGGCGTCACTCTCTCTCC	1732	
Qy	1713	CAAGATCTCCAAAGCCAGTTTCGGGCGGT	TCAGCGCGGGCGCACTGATCGA	1765	
Db	1733	AAAACAGAGAGCGCTCTCCAACGCCACCGT	CATGGCGGGGCACTGATCTA	1785	

RESULT 14  
US-10-437-963-12595  
; Sequence 12595, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

```

; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 12595
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_1B708C.1
US-10-437-963-12595

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Query Match	26.0%;	Score 543;	DB 17;	Length 1662;
Best Local Similarity	62.6%;	Pred. No. 2.5e-108;		
Matches 958;	Conservative 0;	Mismatches 495;	Indels 78;	Gaps 4;
Qy	289	AGCCTCGGGAGGCTCATCTCGCGGATAGTTCGCGCGCGGTGACGTACGGCTGGCGG	348	
Db	148	AGGATCGTCGGCTGTCTTCGCTGATGGTGGCGCGGCATCCAGTACGGCTGGCGG	207	
Qy	349	CTGAGCTCTCCCTCTCTCAAGCCCTACGTGAGACTCTGGGGCTTTCACATGGCCTCACT	408	
Db	208	CTGAGAGTGTCCCTCTCTCGCCCTACTCTCAGACTCTCGGGATTTCCTCACTCGTACGTT	267	
Qy	409	TCATTCATGTGGCTCTCGGCGCCATTTCGCGGCTTAGTGTCAACCGCTGGTTGGCCTG	468	
Db	268	TCCCTGATGATGATCTCGGACCAATCGCTGGATTGTGGTGACCCATCTGTCGGTTAC	327	
Qy	469	TACAGCAGAGGTGTATCATCAGATGGGGAGACGGAGGCGCTTTATTCCTEACAGGCTGC	528	
Db	328	TACAGTCACAGATGCACCATGAAGATGGGCGCGAGGAGGCTTTCATCCTTGTGGGTGC	387	
Qy	529	ATGCTCATCTCGGTTGGCTGCTTGTTCGGATCTCTCGTACAGACTCGGAGCTGCTCTA	588	
Db	388	CTCATCATCTGCACTCTCCGTCATGATCATCGGTTTCTCGGCGACATGAGCACTCACCTC	447	
Qy	589	GGGACACGAAGGAACACTCAGCCTCTACCACGTCTCTGTTGGACGCTGCGATCGTG	648	
Db	448	GGTGACACCAAGACACTCAGCACGTACACGGTCTCTCGCTGGTCGGCGGCACATGGT	507	
Qy	649	TAGCTTCTGGGTTTGGCTGCTTGACTTCTCCAAACAACTGTGAGGCTTCAGACAGT	708	
Db	508	TACATTGTTGGCTTCTGGTTCCTTGACTTCGCTTAAACAACTGTGCCAGGGCGGCTCGT	567	
Qy	709	GCTATGATGGCTGATCT---ATGTGACCATCATGGCGCAAGTCGGCTAACTCATCTTC	765	
Db	568	GCCATGATGGCTGATCTGTACGTGGACACCATGTGCCCCACAGTCGCGCCAGTCGATCTTC	627	
Qy	766	TGTTCTTGGATGGGCTGGGAACAATCCTAGGCTATCTCTCTGCTCCACGAAACAATGG	825	
Db	628	TCCCTGTGGATGGCTATCGGACGCTCTCGGCTACTTGTCCGCGGCCAACGGGAAATGG	687	
Qy	826	CACAAG-----	831	
Db	688	CACGACATTGTGCGCGTGTGGCTAACTATGGTGTTCGTTGATCGCGGCCATTCGTCAGA	747	
Qy	832	TGTTTTCCCTTCCCTTAAACAGAGCGGCTGTGTGAGCCCTGTGCGAACCTGGAAGAGTGCA	891	
Db	748	TGGTTCCATGGCTGAAACCGGGCGGTGTGCGACGCTTCGCGGAACCTCAAGGGCGCC	807	
Qy	892	TTTCTGCTGGCGGTGTTCCTTAGTCTCTGTGCTGTACCGTAACTCCCTGATCTTCGCCAAG	951	
Db	808	TTCTTCAACCGCGGTCTACTATCTGTCGTGAGCATGACGCTGACGATGTACTCTGCCGCAC	867	
Qy	952	GAGGTGCGGTACAGAGCGAAACGAAACCTCCCGACGACGAAGCGCGCGGAGGTGCAG	1011	
Db	868	GAGATGCG-----CTGGACAAGCAGGACGCTCGACACCTCCGCGCGC	909	
Qy	1012	ACTGAGCCTACCGGGCCACTTGGCGTGCTCAAGGGCTTCAAGGACCTGCTCCCGGGATG	1071	
Db	910	GGCGGGTGCCTGGTTCGTGCACTCTTCAAGAGCCTCAGGAACCTGCCCCCGGCATG	969	
Qy	1072	CCGTCCGTGCTCTGTCAGTCGCATCACCTGGCTTTCGTGGTTCCGGTTTCATCCTCTAC	1131	

Db 970 TTCAAAGTCTCGCGTACAGCGCGTCACTGGTGTGTGTTCCCTTTCATCCAGTAC 1029  
QY 1132 GACACCGACTGATGGCGCGGAGATCTAACACGCGGACCCCAAGGGAGCAAGCCCGAG 1191  
Db 1030 AACACCGACTGATGGGACGGAGATCTAACACGCGGAGCCGAGGACCGGCGGCCAAG 1089  
QY 1192 ATCTCGGCGTTCAACGAAGGTTCGAGTCGCGCGTTCGGGCTGCTACTCAATCGGTT 1251  
Db 1090 GCGACGCTGATACGACCGCGGCTCAGGAGGCGCCATGGGCTGCTTCTGCTCGCTC 1149  
QY 1252 ATCTAGGCTCAGCTGCTCTGATCGAGCCATGTGCGGAGGTTCGGCGCGAGGTG 1311  
Db 1150 GCGCTCGGCGTCACTCTCTGATCCCAAGCTGTGCGGAGGTTCGCGGAGGTTCGCG 1209  
QY 1312 GTGTGGGTGACGAGCAACTTCATGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1371  
Db 1210 GTCTGCTCCTCAGCAACTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1269  
QY 1372 TTCTGCTGCTCAGGACTACAGGCTACGTGCGAGGAGCCATCAGG---CGAAGCC 1428  
Db 1270 ATGTGTCTCATGAGAGGTACCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1329  
QY 1429 AGCATCAAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1488  
Db 1330 AGCTCAAGGCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1389  
QY 1489 TACAGCGTCCGCTGCGGCTGACGCGGAGTGTGCGGCGCACCGCGGCGGCGGCGAGGG 1548  
Db 1390 TTCACTGTTTCCATGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1449  
QY 1549 CTGTCCACGCGCTCTCAACATCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1508  
Db 1450 CTGCTCATGCTGCTCTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1509  
QY 1609 GCGGCGCGTGGGCGCGCTGTTGGGAAAGGCAATCCCGGCTTCCGCGTTCGCGCTGCG 1668  
Db 1510 GCGGCGCGTGGGCGCGCTTCAACAAAGGGAACACCGCGGCTTCCGCGATCGCGGCG 1569  
QY 1669 GCTTTCGCTGCTGCGGCGGCTGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1728  
Db 1570 GCTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1629  
QY 1729 CAGTTCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1759  
Db 1630 TCCACGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1660

## RESULT 15

US-10-425-114-22383  
; Sequence 22383, Application US/10425114  
; Publication NO. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingsong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E.  
; APPLICANT: Tabaska, Jack E.  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 22383  
; LENGTH: 1155  
; TYPE: DNA  
; ORGANISM: Oryza sativa nipponbare  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB3479-003-F5\_FLI  
US-10-425-114-22383

Query Match 25.5%; Score 531.8; DB 16; Length 1155;  
Best Local Similarity 80.4%; Pred. No. 6e-106;  
Matches 623; Conservative 0; Mismatches 152; Indels 0; Gaps 0;  
QY 981 CCGGACGACGAAGCGCGGCGGAGGTGAGACTCAGCTACCGGGCCACTTGGCTGCT 1040  
Db 26 CTTCCCAACAATAATCAACGAGCCAGCTGAGCTGAGGCACTGGTCCACTAGCAGTGT 85  
QY 1041 CAAGGCTTCAAGGACCTGCTCCCGGATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1100  
Db 86 GAAAGGCTTCAGAAACTTACTACTTGGGATGCTTCTGCTTATTTGTAAGTGGCTTAC 145  
QY 1101 CTGGCTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1160  
Db 146 CTGGTGTCTTGGTTCCTCATCTCTACGACACGACTGAGTGGGCGGAGATCTA 205  
QY 1161 CCACGCGACCCCAAGGGGAGCAACGCCAGATCTCGGCTTCAACGAAGGTGCCAGT 1220  
Db 206 CCACGCTGACCCAAAGGAACTGATCTCTCAGATCAGGCTTCAACCAAGGCTGCAGGCG 265  
QY 1221 CGCGGCTTCGGGCTGCTACTCACTCGGTATTCTAGGCTTCACTGCTGCTGCTGCTG 1280  
Db 266 AGGTGCATTTGGCTGCTACTGATTCGATTTGCTAGGATTCAGCTCATTTCTGATTTGA 325  
QY 1281 GCCCATGTCCCGAAAGTCCGGCCGAGGCTGTGTGGGTGACGAGCAACTTCATGCTGTG 1340  
Db 326 ACCAATGTCCGGAAGTCCGGCCAAAGGTGTGTGGGTGACGAGCAATTTCTCGTCTG 385  
QY 1341 CTTGCGCATGCGGCGCACCGGCTGATCAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1400  
Db 386 CATCGCATGCTGCAACTGCACTGATCAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 445  
QY 1401 CTTGCGAGGACGCTACCGGAAACGCGAGCATCAAGCCGCTGCTGCTGCTGCTGCTGCTG 1460  
Db 446 TGTTCAGAAAGCCATCACTGACAGCAAGAGCATCAAGGCTGTCTGCTGCTGCTGCTG 505  
QY 1461 CTTCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1520  
Db 506 GTTCTTGGAGTCCCTCTCGCGTCTGTACAGTGTTCCTTCGCAAGTGCAGTGCAGGCG 565  
QY 1521 GCGGCGCACCGGCGGCGGCGGAGGCTGTGACACCGGCTGCTGCTGCTGCTGCTGCTGCTG 1580  
Db 566 AGCGGCGCATAGAGGCGGTGGCCAAAGGCTCTGTACCGGCGCTGCTGCTGCTGCTGCTG 625  
QY 1581 CATCCCTCAGGTGATCATCGGCTGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1640  
Db 626 CATCCCTCAGGTGATCATCGGCTGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 685  
QY 1641 CAACATCCCGGCTTCCGGGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1700  
Db 686 GAACATCCCGGCTTCCGGGCTGCGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTG 745  
QY 1701 GTTCTGCTGCGGCGGAGTCTCAAGCGGCGAGTTCGCGGCGGCTGCGGCGGCGGCGG 1755  
Db 745 ATTCTGCTGCGGCGGAGTCTCAAGCGGCGAGTTCGCTGCTGCTGCTGCTGCTGCTGCTG 800

Search completed: November 7, 2004, 14:38:30  
Job time: 1044 secs

GenCore version 5.1.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 7, 2004, 05:29:17 ; Search time 6565 Seconds  
(without alignments)  
11589.666 Million cell updates/sec

Title: US-09-679-687B-1  
Perfect score: 2088  
Sequence: 1 GCAAGACACCTCCTCACTT.....AAAAAAAAAAAAAAAAAAAAA 2088

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_htc:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gsal:\*  
9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2088	100.0	2088	3	AY106212 Zea mays
2	850.6	40.7	902	6	CD440318 ELOIN0553
3	790.4	37.9	895	6	CD441187 ELOIN0553
4	630.6	30.2	1071	7	CK162807 FGAS01551
5	546	26.1	869	6	CD434724 ELOIN0327
6	539.6	25.8	847	6	CB647418 OSUNE010F
7	531.8	25.5	654	6	CA195914 SCEZAD108
8	523.6	25.1	705	5	BU925783 MCSA174E1
9	518.6	24.8	811	6	CB659941 OSUNE001E
10	516.4	24.7	843	6	CB661694 OSUNE004P
11	508	24.3	638	6	CD236385 SSI_33_G1
12	495	23.7	589	6	CA399941 ELOIN0327
13	493.8	23.6	769	6	CB678068 OSUNE015J
14	490.8	23.5	742	6	CB618707 OSIT1E02M
15	488.8	23.4	719	5	BU925792 MCSA179A0
16	484.8	23.2	496	5	BQ538253 MEST599-A
17	480.2	23.0	581	2	BE361547 DGL_81_H0
18	476.8	22.8	657	6	CF325368 JMT1--04-
19	463	22.2	998	7	CK162767 FGAS01536
20	457.2	21.9	694	6	CD881813 FI.104E23
21	445	21.3	538	6	CA220149 SCRFL402
22	443.8	21.3	657	7	CNI50206 WOUND1_67
23	437.6	21.0	656	6	CD879901 AZO4_106L
24	433.8	20.8	539	6	CA163799 SCRURZ308

25	433.2	20.7	704	6	CD884481	FL116M07
26	432.4	20.7	594	2	BF478755	WHE2013_C
27	429	20.5	532	7	CF630902	ZMRWS46_0
28	429	20.5	647	1	AV925143	AV925143
29	425.8	20.4	533	7	CK369825	ZMRWS485
30	422.6	20.2	592	5	BQ743802	WHE4108_C
31	422.4	20.2	526	6	CD970384	QAD16e03
32	422.4	20.2	526	6	CD970430	QAD17b09
33	420.6	20.1	617	4	BJ477966	BJ477966
34	416.4	19.9	482	4	BG837732	Zm10_05d0
35	414.2	19.8	700	1	AL508285	AL508285
36	411.8	19.7	518	2	BE360821	DGI_67_H0
37	411.6	19.7	828	4	BI953334	HVSMEM001
38	411.4	19.7	795	7	CO522314	3530_1_14
39	411.2	19.7	828	9	CC692415	OGUCF61TH
40	409.8	19.6	768	7	CO527407	3530_1_18
41	409.4	19.6	731	7	CK124551	BES182410
42	403.8	19.3	587	6	CA222528	SCBFL405
43	402.4	19.3	516	7	CK371610	ZMRWS005
44	396.2	19.0	757	8	BZ638091	OGCAR67TC
45	393	18.8	582	6	CD057532	HO15G16S

## ALIGNMENTS

RESULT 1  
AY106212  
LOCUS Zea mays PC0103031 mRNA sequence.  
DEFINITION Zea mays PC0103031 mRNA sequence.  
ACCESSION AY106212  
VERSION AY106212.1 GI:21209290  
KEYWORDS HTc.  
SOURCE Zea mays  
ORGANISM Zea mays

REFERENCE 1 (bases 1 to 2088)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD clade; Panicoideae; Andropogoneae; Zea.  
AUTHORS Hayne, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whittitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.

TITLE Maize Mapping Project/Dupont Consensus Sequences for Design of Overgo Probes

JOURNAL Unpublished (2002)  
REFERENCE 2 (bases 1 to 2088)  
Coe, E.H.

JOURNAL Direct Submission  
TITLE Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA  
COMMENT If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSI, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.

FEATURES  
source

1..2088  
/organism="Zea mays"  
/mol\_type="mRNA"  
/db\_xref="MaizeDB:635944"  
/db\_xref="taxon:4577"  
/clone\_lib="Maize Mapping Project/Dupont Consensus Library"  
/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed Dupont contigs; this resource was assembled by Dupont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"

ORIGIN

Query Match 100.0%; Score 2088; DB 3; Length 2088;



QY 1144 ATGGCCGGGAGATCTACCAAGCGCACCCCAAGGGAGCAACGCCAGATCTCGGCGTTC 1203

[illegible]



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Db      363 ATGGCTGATTATATCAGCCAGCATGACACCGAGTGCAGCAAAATTCATATCTCTGTTCTGG 422
Qy      775 ATGGCGCTGGGAACATCTAGACTACTCTCTGGCTCCACGACAAATTTGGACAGTGG 834
Db      423 ATGGCACTGGGAATATCTTAGATATCTATCTGGTTCCACAAATTAACATGGCACAAGTGG 482
Qy      835 TTTCCTCTCTTAAACGAGCGCTCTGTGAGGCTGTGCGAAACCTGAAAGGTGCATTT 894
Db      483 TTTCCTCTCTCCGGAACAGGCTTCTGTGAGCTGCGCAATCTGAAAGCGCATTT 542
Qy      895 CTGGTGGCGGTGTGTCTAGTCTCTGCTGCTGAGAGTAACTGATCTTCCGCCAAGGAG 954
Db      543 CTGGTGGCGGTGTGTCTGCTGCTTCTGTTGGTGATTAACCGTGTATCTTCCCAAGGAG 602
Qy      955 GTGCCGTACAGACGGAACAGAAACCTCCCGACGACGAAAGCGCGGCGAGTCCAGACT 1014
Db      603 ATACCGTACAGCGATTGGCCCCCTCC---CAAACAAGGCCAAATGGCCAGTTGAAGTC 659
Qy      1015 GAGCCTACCGGCGCATCTCCGCTGCTCAAGGGCTTCAAGGACTGCTGCTCCCGGAGTGGC 1074
Db      660 GAGCCACCGGCGCTCGCCGCTCTTCAAGGCTTCAAGGACTTGCCTCTGGAATGCGG 719
Qy      1075 TCGTGTCTCTCTGTGACTGCCATCACTGCTGCTTCTGTTGTTCCGTTCTATCTCTACGAC 1134
Db      720 TAGTGTCTCTGTACCGCTCACTGCTGCTGCTGTTCTCTCTCTCTGTTACCTGACGAC 779
Qy      1135 ACCGACTGATGGCGCGGAGATCTACACGCGACCCCAAGGGAGCAACGCCAGATC 1194
Db      780 ACCGACTGATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 838
Qy      1195 TCGGGGTTCACGAGAGTGTCCGAGTCCGAGTCCGCGGTTCGGGCTGCTACTCACTCGTTATT 1254
Db      839 AACGGGTTCAGGAGGTGTCCGAGTCCGAGTCCGCGGTTCGGGCTGCTACTCACTCGTTATT 1314
Qy      1255 CTAGGGTTCAGTCTGTTCTGATCGAGCCCATGTGCGGAGAGTCCGCGGAGGAGTGGTG 1314
Db      899 CTGGGGTTCAGTCTGTTCTGATCGAGCGCTGTGCAAGAGG-CTAGCCGCGGTGGTG 957
Qy      1315 TCGGTGACGAGCAACTCATGTCTGC 1341
Db      958 TGGGTGTC-AGCAACTTCTCCGCTGTC 983

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RESULT 5
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LOCUS      ELOIN0327D07.b Endospem_3 Zea mays cDNA, mRNA linear EST 03-JUN-2003
DEFINITION CD434724
ACCESSION  CD434724.1 GI:31350367
VERSION    EST.
KEYWORDS   Zea mays
SOURCE     Zea mays

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ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

```

```

REFERENCE
1 (bases 1 to 669)
Lai,J., Dey,N., Kim,C.S., Becraft,P., Larkins,B., Linton,E. and
Messing,J

```

```

Sequencing of the maize endospem ESTs
Unpublished (2002)
Contact: Lai, Jinsheng

```

```

Dr. Joachim Messing's lab
Waksman Institute, Rutgers University
190 Frelinghuysen Rd., Piscataway, NJ 08854, USA
Tel: 732-445-3801
Fax: 732-445-5735
Email: jlai@waksman.rutgers.edu

```

```

Seq primer: T3.
Location/Qualifiers
1..669
/organism="Zea mays"
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/cultivar="W22"

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FEATURES
source

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/db_xref="taxon:4577"
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## ORIGIN

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Query Match      26.1%; Score 546; DB 6; Length 669;
Best Local Similarity 94.0%; Pred. No. 1.5e-98;
Matches 624; Conservative 0; Mismatches 30; Indels 10; Gaps 5;
Qy      1390 TACCACGGGTACGTGACGAGCGCCATCACGCGCAACGCCAGCATCAAGGCGCTCTGCGCTC 1449
Db      10 TACCACGGGTACGTGACGAGCGCCATCACGCGCAACGCCATCAAGGCGCTCTGCGCTC 69
Qy      1450 GTCTCTTTCGCTTCTTGGGGTTCCTCTGCCATCTCTAGACGCTCCGT-TCGCGGT 1508
Db      70 GTCTCTTTCGCTTCTTGGGGTTCCTCTGCCATCTCTAGACGCTCCGTCTCGCGGA 129
Qy      1509 GACGCGCAGCTGGCGGCCACCCGGGCGGGGCGAGGGCTGTGCAACCGGCGCTCAA 1568
Db      130 GACGCGCAGCTGGCGGCCACCCGGGCGGGGCGAGGGCTGTGCAACCGGCGCTCAA 189
Qy      1569 CATCTCCATCGTCATCTCTCAGTGTATCATGCGCTGGGCGCGCGCTGGGACGCGCT 1628
Db      190 CATCTCCATCGTCATCTCTCAGTGTATCATGCGCTGGGCGCGCGCTGGGACGCGCT 249
Qy      1629 GTTCGGGAAGGGCAACATCCGGGCTTGGGCTGGGCTGGGCTTCCGCTCTCGTGGGCGG 1688
Db      250 GTTCGGGAAGGGCAACATCCGGGCTTGGGCTGGGCTTCCGCTCTCGTGGGCGG 309
Qy      1689 CGTCTGGGCGTGTCTCTGCTGCCAAGATCTCCAAGCGCAGTTCCGGGCGCTCAAGCGC 1748
Db      310 CGTCTGGGCGTGTCTCTGCTGCCAAGATCTCCAAGCGCAGTTCCGGGCGCTCAAGCGC 369
Qy      1749 GGGCGGCACATGATCGAACCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 1808
Db      370 GGGCGGCACATGATCGAACCC---CCGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 426
Qy      1809 GTATGTTG-TTGAGAGTTGAACAGAACCATGATGTGTCTTCTGTAGTTCT----GTT 1863
Db      427 GTATGTTGAGAGTCAGTTGAACAGAACCATGATGTGTCTTCTGTAGTTCTGTAGTT 486
Qy      1864 GTTGTGTCGATCGATGGCGTGTGGTGGCAGCGTGGGCAAGCGAGGCGAGTGGCGG 1923
Db      487 GTTGTGTCGTCGTCTGGTTCGATCGATAGGCTGCGTGGGCAAGCGAGGCGAGTGGCGG 546
Qy      1924 ATCCAAAAAAGGCCCATTCGATCAATCAATGTGTAGTAGTACAACTAGACGATGATG 1983
Db      547 ATCC-AAAAAAGGCCCATTCGATCAATCAATGTGTAGTAGTACAACTAGACGATGATG 605
Qy      1984 TTCACATCATTTGCTTTAATACATACCGGTTTCTATTGTTTAAAAAATAAAAAA 2043
Db      606 TTCACATCATTTGCTTTAATACATACCGGTTTCTATTGCTATTACAAAAAATAAAAAA 665
Qy      2044 AAAA 2047
Db      666 AAAA 669

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RESULT 6

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CB647418

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LOCUS

```

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DEFINITION

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OSJNEB10F12.f OSJNEB Oryza sativa (japonica cultivar-group) cDNA

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```

CB647418

```

```

ACCESSION

```

```

VERSION

```

```

CB647418.1 GI:29642411

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```

KEYWORDS

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```

SOURCE

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ORGANISM

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```

Oryza sativa (japonica cultivar-group)

```

```

Oryza sativa (japonica cultivar-group)

```

```

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

```

```

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

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Ehrhartoideae; Oryzaceae; Oryza.

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CB647418      847 bp      mRNA linear      EST 08-APR-2003
OSJNEB10F12.f OSJNEB Oryza sativa (japonica cultivar-group) cDNA
Clone OSJNEB10F12 5', mRNA sequence.

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CB647418

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CB647418.1 GI:29642411

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EST.

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Oryza sativa (japonica cultivar-group)

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```

Oryza sativa (japonica cultivar-group)

```

```

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

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Ehrhartoideae; Oryzaceae; Oryza.

```

```

REFERENCE
AUTHORS      Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
              Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
TITLE        Large-scale identification of ESTs involved in the interaction
              between rice and Magnaporthe grisea
JOURNAL      Unpublished (2003)
COMMENT      Contact: Rod Wing
              Arizona Genomics Institute
              University of Arizona
              Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
              85721-0088, USA
              Tel: 520 626 3967
              Fax: 520 621 9288
              Email: http://genome.arizona.edu
PCR Primers  FORWARD: gta aaa cga cgg cca gtc
              BACKWARD: gga aac agc tat gac cat g
              Plate: 10 row: F column: 12
              Seq primer: gta aaa cga cgg cca gtc.
              Location/Qualifiers
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              /tissue_type="Leaf"
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              /lab_host="DH10B"
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              /note="Vector: pBluescript II KS +; Site 1: EcoRI; Site 2:
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Query Match      25.8%; Score 539.6; DB 6; Length 847;
Best Local Similarity 78.0%; Pred. No. 2.8e-97;
Matches 663; Conservative 0; Mismatches 184; Indels 3; Gaps 1;
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QY      748  GCGGTAACTCCATCTTCTGTTCITGGATGGCGCTGGGAACATCCTAGGCTACTCTCT 807
DB      61  ACAGTAACTCCATCTCTGTTCTTGGATGGAATGGGAACATCCTAGGATACTCTCT 120
QY      808  GGCTCAGCAAAATGGCAGAGTGGTTCCTTCTTAAACGAGCGCTGCTGTGAG 867
DB      121  GGTTCACAAACAAATGGCAGAGTGGTTCCTTCTTAAACGAGCGTGTCTGAAA 180
QY      868  GCGTGTGCAACTCAAGGTGCATTTCTGTGGCGGTGGTTCCTAGTCTGTGCTG 927
DB      181  GTTTGTGCAATTTGAAGGTGCATTTCTGTGGCTGTGATTTTCTCTGCTGCTG 240
QY      928  ACGGTAACCTGATCTTCCCAAGAGTGGCTGTACAGAGCGAGCACTCCCGACG 987
DB      241  GTTATAACTCTGATATTTGCCAAGAGTTCCTTCAAGAGAAATGACGCGCTCC 297
QY      988  ACGAAGGCGCGGCGGAGTCCAGACTGAGCTACCGGGCCACTTGCCTGCTCAAGGC 1047
DB      298  ACAAAATCAACAGCAGCAGTGAAGCTGAGCACTGTCCTAGCAGTGTGAAGGC 357
QY      1048  TTCAAGGACCTCCCTCCCGGATGCGGTCCGTGCTCTCGTACTGCCATCACTGGCTT 1107
DB      358  TTCAGAACTTACCTACTGGGATGCTTCTGTGCTTATTGTGACTGGCTTACCTGTTG 417
QY      1108  TCGTGGTTCCTCTCTACACACCGACTGGATGGCCGGAGATCTACACAGGC 1167
DB      418  TTTTGTGTTCCCAATTCATCTCTTACACACTGACTGGATGGCCGGTGAATACACGGT 477
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Db      478  GACCAAGGAACTGATCCTCAGATCGAGGCTTTCARACAGGTTGTGAGGCGAGTGCA 537
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Db      538  TTTGGCTGCTACTGAATTCGATTTGTAGGATTCAGCTCATTTCTTGATTGAACCAATG 597
QY      1288  TCCCGAAGGTCCGCGGAGGTGGTGGGTGAGAGCAACTTCATGCTCTGGTGGTCC 1347
Db      598  TCCCGAAGGTCCGCGGAGGTGGTGGGTGAGAGCAACTTCCTGCTGTGATCGCC 657
QY      1348  ATGCGCGCCACCGCGCTGATCAGCTTCTGGTGGTTCACGGACTACACGGGTACGTGCAG 1407
Db      658  ATGGCTGCAACTGCACTGATCAGCTTCTGGTCACTCAAGGACTTCATGGAACCTGTT 717
QY      1408  GAGGCATCACCGCAACGCCAGCATCAAGCGCTCAAGCGCTCTGCTCGCTCTCTG 1467
Db      718  AAAGCCATCACTGCAGCAAGAGCATCAAGGCTGTCTGCTCGCTCTCTTTCGCTTCT 777
QY      1468  GCGCTCCCTCTCGCCATCCTGTACAGCGTCCCGTTCGCGGTGACGCGCAGCTGCGGCC 1527
Db      778  GAGTCCCTCTCGCGTTCCTGTACAGTGTTCCTTCGCACTGACGCGCAAAATAGCGCC 837
QY      1528  ACCCGGGCG 1537
Db      838  ACTAGAGGGG 847

RESULT 7
CA195914
LOCUS     SCEZAD1082D06.g AD1 Saccharum officinarum cDNA clone SCEZAD1082D06
          5', mRNA sequence.
ACCESSION CA195914
VERSION    CA195914.1 GI:35224640
KEYWORDS   EST
SOURCE     Saccharum officinarum
ORGANISM   Saccharum officinarum
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
           clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
           complex.
REFERENCE  1 (bases 1 to 654)
AUTHORS   Vetore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
TITLE     The libraries that made SUCEST
JOURNAL   Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
COMMENT   Contact: Arruda P
           Centro de Biologia Molecular e Engenharia Genetica
           Universidade Estadual de Campinas
           Caixa Postal 6010, 13083-970, Campinas SP, Brazil
           Tel: 55 19 3788 1137
           Fax: 55 19 3788 1089
           Email: parada@unicamp.br
           Clone distribution: clone distribution information can be found
           through the Brazilian Clone Collection Center (BCCC) at
           http://www.bcccenter.fcav.unesp.br
           Plate: 082 row: D column: 06
           Seq primer: T7 Promoter Primer.
FEATURES  Location/Qualifiers
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           /db_xref="taxon:4547"
           /clone="SCEZAD1082D06"
           /lab_host="DH10B"
           /clone_lib="AD1"
           /note="Organ: seedlings inoculated with Gluconacetobacter
           diazotrophicus; Vector: pSPori; Site 1: SalI; Site 2:
           NotI; An unidirectional cDNA library generated from
           [seedlings inoculated with Gluconacetobacter
           diazotrophicus]. cDNA was prepared from polyA+ mRNA using
           Superscript Plasmid System Kit (Invitrogen). The
           double-strand cDNAs were fractionated in a sepharose
           CL-2B 40cm-columns and fragments sizing between 0.8 and

```

1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at <http://sucst.lad.ic.unicamp.br/public>

## ORIGIN

Query Match	25.5%; Score 531.8; DB 6; Length 654;	
Best Local Similarity	89.0%; Pred. No. 1e-95;	
Matches 585; Conservative	0; Mismatches 69; Indels 3; Gaps 1;	
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Db	1	CGCTGGGAACAATCCTAGGCTATCTCTGGTTCCAAACAATGGCAACAATGGTTTC 60
QY	839	CCTTCTTTAAACGAGCGGCTGCTGTGAGCCCTGTGCGAACCTGAAAGGTGCAATTTCTCG 898
Db	61	CCTTCTCTCAAAACAAATGCGTGTGTGAAGCCCTGTGCAAACTGAAAGGTGCAATTTCTCG 120
QY	899	TGGCCGTGTGTTCTCTAGTCCCTGCTGACGGTAAACCTGATCTTTCGCCAAGGAGTGC 958
Db	121	TGGCTGTGTGTCTCTAGTCAATATGTTGGCGTAACCTTGATCTTCGTGAAGGAAGTAC 180
QY	959	CGTACAGAGCAACGAGAACCTCCGACGACGAAGCCGGCGGAGGTGCGACATCGAGC 1018
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Db	238	CTACCGGGCCACTTGCAAGTGTGAAGGGTTCAAGAACTTGCCCCCGGGATGCGCTCCG 297
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QY	1259	GGTTCAGCTCGTTCTGTATCGAGCCCATGTGCGGAAGGTTCGGCCGAGGGTGTGTGG 1318
Db	478	GATTGAGCTCATCTCTGATCGAGCCCATGTGTCGGAAGCTCGGGCCGAGGGTGTGTGG 537
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QY	1379	CGCTCAGGACTTACCAAGGTTACGTGTCAGGACGCCATCACCGCAACGCCAGCATCA 1435
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RESULT 8	BU925783	705 bp	linear	EST 06-JUN-2003
LOCUS	BU925783		mRNA	
DEFINITION	MCSA174E10	Maturing Sugarcane Stem Lambda ZIPLOX Library (MCS)		
	Saccharum sp.	cDNA clone MCSA174E10 5' similar to PST type 6, mRNA		
	sequence.			
ACCESSION	BU925783			
VERSION	BU925783.1	GI:31442678		
KEYWORDS	EST.			
SOURCE	Saccharum sp.			
ORGANISM	Saccharum sp.			
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Saccharum.			
REFERENCE	1 (bases 1 to 705)			
AUTHORS	Casu, R.E., Grof, C.P.L., Rae, A.L., McIntyre, C.L., Dimmock, C.M. and Manners, J.M.			
TITLE	Identification of a novel sugar transporter homologue strongly expressed in maturing stem vascular tissues of sugarcane by			

expressed sequence tag and microarray analysis  
Plant Mol. Biol. 52 (2), 371-386 (2003)  
22740598  
12856943  
Contact: Rosanne E. Casu  
Commonwealth Scientific and Industrial Research Organisation  
Division of Plant Industry  
Long Pocket Laboratories, 120 Meiers Rd, Indooroopilly, QLD, 4068,  
Australia  
Tel: 61 7 3214 2364  
Fax: 61 7 3214 2881  
Email: Rosanne.Casu@csiro.au  
Bases 1-17 (GTGACCCACGGCCG): Sali adapter  
Seq primer: T7 sequencing primer  
High quality sequence stop: 705.

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16. cloning. The cDNA was clon
17. of the Lambda Z1XPLO phage
18. Constructed by Rosanne E.

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Db	558	CCCCGCGTTCCGCGCTGNCGTCCGGGTTTCGCTTCATCGCGCGCTCGTGGCGCTTCCT	617
QY	1707	GCTGCCCAAGATCTCCAAGCGCCAGTTCGCGCCCTGCA--GCGCGCGCGCCACTGATCG	1764
Db	618	GCTGCCAAATCTCCAAGCGCCAGTTCAGGCGCCCTTAAGCGCCGCGNCACTGATCG	677
QY	1765	AACCCGCGCGG	1775
Db	678	AGCCGCGCG	688
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DEFINITION	clone OSJNEd01E20 5', mRNA sequence.		
ACCESSION	CB659941		
VERSION	CB659941.1 GI:29663666		
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SOURCE	Oryza sativa (japonica cultivar-group)		
ORGANISM	Oryza sativa (japonica cultivar-group)		
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	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;		
	Ehrhartoidae; Oryzeae; Oryza.		
REFERENCE	1 (bases 1 to 811)		
AUTHORS	Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E., Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.		
TITLE	Large-scale identification of ESTs involved in the interaction between rice and Magnaporthe grisea		
JOURNAL	Unpublished (2003)		
COMMENT	Contact: Rod Wing Arizona Genomics Institute University of Arizona Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ 85721-0088, USA Tel.: 520 626 3967 Fax: 520 621 9288 Email: http://genome.arizona.edu		
FEATURES			
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```

REFERENCE
AUTHORS      Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
              Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
TITLE        Large-scale identification of ESTs involved in the interaction
              between rice and Magnaporthe grisea
JOURNAL      Unpublished (2003)
COMMENT      Contact: Rod Wing
              Arizona Genomics Institute
              University of Arizona
              Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
              85721-0088, USA
              Tel: 520 626 3967
              Fax: 520 621 9288
              Email: http://genome.arizona.edu
PCR Primers  FORWARD: gta aaa cga cgg cca gtc
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Best Local Similarity 77.6%; Pred. No. 3.9e-88;
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            Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
            Kuarna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
            Large-scale identification of ESTs involved in the interaction
            between rice and Magnaporthe grisea
            Unpublished (2003)
            Contact: Rod Wing
            Arizona Genomics Institute
            University of Arizona
            Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
            85721-0088, USA
            Tel: 520 626 3967
            Fax: 520 621 9288
            Email: http://genome.arizona.edu
PCR Primers  FORWARD: gta aaa cga cgg cca gtc
            BACKWARD: gga aac agc tat gac cat g
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